

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 12, 2003, 08:39:44 ; Search time 16 Seconds  
(without alignments)  
951.430 Million cell updates/sec

Title: US-09-905-810-2  
Perfect score: 1268  
Sequence: 1 MAARRSQRGRGRRGEPCTAL.....PWAHLKAAPLTYFGLFQVH 249

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

searched: 248812 seqs, 61136040 residues  
al number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA:\*
- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW PUB.pep.\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT NEW PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW PUB.pep.\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW PUB.pep.\*
  - 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
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  - 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW PUB.pep.\*
  - 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
  - 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW PUB.pep.\*
  - 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	249	10	US-09-905-810-2
2	1268	100.0	249	10	US-09-782-980-44
3	1066	84.1	273	10	US-09-742-454A-2
4	1066	84.1	273	10	US-09-883-777-2
5	1020	80.4	225	10	US-09-905-810-1
6	116	9.1	409	10	US-09-813-329-6
7	105.5	8.3	406	10	US-09-813-329-4
8	104	8.2	409	10	US-09-813-329-2
9	92.5	7.3	208	10	US-09-027-287-39
10	92.5	7.3	208	10	US-09-252-656B-39
11	91.5	7.2	240	9	US-09-967-604-6
12	91.5	7.2	240	9	US-10-151-882-45
13	91.5	7.2	240	10	US-09-027-287-2
14	91.5	7.2	240	10	US-09-252-656B-2
15	91.5	7.2	240	12	US-10-066-209-4
16	90	7.1	660	12	US-10-115-178-1
17	88	6.9	373	9	US-10-174-590-372
18	88	6.9	373	9	US-10-176-759-372
19	88	6.9	373	9	US-10-175-737-372

20	88	6.9	373	9	US-10-173-706-372	Sequence 372, App
21	88	6.9	373	9	US-10-175-738-372	Sequence 372, App
22	88	6.9	373	9	US-10-175-752-372	Sequence 372, App
23	88	6.9	373	9	US-10-176-482-372	Sequence 372, App
24	88	6.9	373	9	US-10-176-757-372	Sequence 372, App
25	88	6.9	373	9	US-10-176-913-372	Sequence 372, App
26	88	6.9	373	9	US-10-180-552-372	Sequence 372, App
27	88	6.9	373	9	US-10-180-557-372	Sequence 372, App
28	88	6.9	373	9	US-10-173-700-372	Sequence 372, App
29	88	6.9	373	9	US-10-174-572-372	Sequence 372, App
30	88	6.9	373	9	US-10-174-579-372	Sequence 372, App
31	88	6.9	373	9	US-10-174-582-372	Sequence 372, App
32	88	6.9	373	9	US-10-174-588-372	Sequence 372, App
33	88	6.9	373	9	US-10-175-739-372	Sequence 372, App
34	88	6.9	373	9	US-10-175-740-372	Sequence 372, App
35	88	6.9	373	9	US-10-175-743-372	Sequence 372, App
36	88	6.9	373	9	US-10-176-488-372	Sequence 372, App
37	88	6.9	373	9	US-10-176-492-372	Sequence 372, App
38	88	6.9	373	9	US-10-176-747-372	Sequence 372, App
39	88	6.9	373	9	US-10-176-750-372	Sequence 372, App
40	88	6.9	373	9	US-10-176-985-372	Sequence 372, App
41	88	6.9	373	9	US-10-176-987-372	Sequence 372, App
42	88	6.9	373	9	US-10-176-991-372	Sequence 372, App
43	88	6.9	373	9	US-10-176-992-372	Sequence 372, App
44	88	6.9	373	9	US-10-176-993-372	Sequence 372, App
45	88	6.9	373	9	US-10-184-658-372	Sequence 372, App

ALIGNMENTS

RESULT 1  
US-09-905-810-2  
; Sequence 2, Application US/09905810  
; Patent No. US20020015703A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; APPLICANT: RENNERT, Paul  
; TITLE OF INVENTION: Antagonists of Tweak and of Tweak Receptor and Their Use to Treat Immunological Disorders  
; FILE REFERENCE: A068 US  
; CURRENT APPLICATION NUMBER: US/09/905,810  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: PCT/US00/01044  
; PRIOR FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-905-810-2

Query Match	100.0%;	Score	1268;	DB	10;	Length	249;
Best Local Similarity	100.0%;	Pred. No.	6.4e-108;	Mismatches	0;	Indels	0;
Matches	249;	Conservative	0;			Gaps	0;
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Db	1	MAARRSQRGRGRRGEPCTALLVPLALGLGUALACGLLLAVVLSGRASLSAQEPAGEEL	60				
Qy	61	VAEEDQPSSELPNPTESQDPAFLNRLVRRSPAPKGRKTRARRAJAAHYEVHPRQD	120				
Db	61	VAEEDQPSSELPNPTESQDPAFLNRLVRRSPAPKGRKTRARRAJAAHYEVHPRQD	120				
Qy	121	GAQAGVDTGTVSGWEAEARINSSPLRYNRQIGEFIVTRAGLYLYCQVHFDGKAVYKLD	180				
Db	121	GAQAGVDTGTVSGWEAEARINSSPLRYNRQIGEFIVTRAGLYLYCQVHFDGKAVYKLD	180				
Qy	181	LLVDGVIALRCLEEFSTAAASSLGFQRLQCVSGLLALRPGSSLRIRTLPAWHLKAAPFL	240				
Db	181	LLVDGVIALRCLEEFSTAAASSLGFQRLQCVSGLLALRPGSSLRIRTLPAWHLKAAPFL	240				



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OM protein - protein search, using sw model

Run on: April 12, 2003, 08:39:12 ; Search time 36 Seconds  
(without alignments)  
921.650 Million cell updates/sec

Title: US-09-905-810-2

Perfect score: 1268

Sequence: 1 MAARSRQRRRRGFBGTAL.....PWAHLKAAFFLYFGLFQVH 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

.l number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 101002.\*

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23: /SID32/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1268	100.0	249 20	AA093169 Human tumour necro
2	1268	100.0	249 21	AA07526 Amino acid sequenc
3	1268	100.0	249 21	AA095338 Human PRO207 antit
4	1268	100.0	249 23	AA086129 Human PRO207 polyp
5	1268	100.0	284 19	AA047525 Homo sapiens tumou
6	1268	99.8	249 19	AA029745 TNF related endoth
7	1265	99.8	249 22	AA000891 Human TREPA (TNF r
8	1066	84.1	273 22	AA003499 TWEAK extracellular
9	1062	83.8	208 20	AA093590 Human TNRL3 protei
10	1020	80.4	225 19	AA047524 Mus musculus tumou

11	1020	80.4	225	21	AA07527	Amino acid sequenc
12	968	76.3	211	20	AA093591	Mouse TNRL3 protei
13	792	62.5	189	19	AA029746	TNF related endoth
14	792	62.5	189	22	AA000892	Human UL4flag TREP
15	761	60.0	146	22	AA000895	Human TREPA (TNF r
16	116	9.1	325	22	AB067553	Drosophila melanog
17	116	9.1	409	23	AA077718	Drosophila melanog
18	108.5	8.6	211	21	AA058215	Canine mature CD15
19	108.5	8.6	260	21	AA058215	Canine CD154. Can
20	105.5	8.3	406	23	AA077717	Drosophila melanog
21	104	8.2	409	23	AA077717	Drosophila melanog
22	100	7.9	220	22	AA062340	Gp120 V3 loop-CD15
23	96	7.6	234	22	AA062339	Gp120 V3 loop-CD15
24	95.5	7.5	254	16	AA064190	Human 4-1BB-L poly
25	95.5	7.5	254	18	AA026657	Human 4-1BB ligand
26	95.5	7.5	254	23	AB075953	Human cytokine 4-1
27	94.5	7.5	240	23	AA013680	Human HVEM-binding
28	93.5	7.4	876	22	AB000217	Novel human diagno
29	93	7.3	1428	21	AA097033	Caspase 8-interact
30	92.5	7.3	208	20	AA031886	Human apoptosis in
31	92.5	7.3	208	20	AA06474	Human apoptosis in
32	92.5	7.3	208	21	AA018619	Partial human apop
33	92.5	7.3	208	23	AB081653	Human partial apop
34	92.5	7.3	240	23	AA013681	Human HVEM-binding
35	91.5	7.2	240	18	AA032255	Human apoptosis in
36	91.5	7.2	240	19	AA040362	Human Fas ligand-1
37	91.5	7.2	240	20	AA031885	Human apoptosis in
38	91.5	7.2	240	20	AA06473	Human apoptosis in
39	91.5	7.2	240	20	AA095033	Tumour necrosis fa
40	91.5	7.2	240	21	AA018618	A human apoptosis
41	91.5	7.2	240	22	AA078921	Human TL4. Homo s
42	91.5	7.2	240	22	AA048938	Human TL4 liver fu
43	91.5	7.2	240	23	AB081648	Human apoptosis in
44	91.5	7.2	240	23	AA013677	Human herpes virus
45	91.5	7.2	240	23	AA013679	Human HVEM-binding

#### ALIGNMENTS

RESULT 1  
AA093169  
ID AA093169 standard; Protein; 249 AA.  
XX  
AC AA093169;  
XX  
DT 15-JUL-1999 (first entry)  
XX  
DE Human tumour necrosis factor Apo-3 ligand protein sequence.  
XX  
KW Human; tumour necrosis factor; Apo-3 ligand; lymphotoxin; apoptosis;  
KW NF-kappaB-dependent transcription; JNK/SAPK-dependent response;  
KW cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO9919490-A1.  
XX  
PD 22-APR-1999.  
XX  
PF 09-OCT-1998; 98WO-US21407.  
XX  
PR 17-DEC-1997; 97US-0069862.  
XX  
PR 10-OCT-1997; 97US-0062037.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Marsters SA, Pitti R;  
XX  
DR WPI: 1999-287982/24.  
XX  
DR N-PSDB; AA056000.  
XX  
PT New human Apo-3 ligand (a tumour necrosis factor) homologue

XX PS Claim 1; Fig 1; 74pp; English.

XX CC The present sequence represents a human tumour necrosis factor (TNF) and lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has CC cytostatic activity. Apo-3 ligand can be used to induce apoptosis in CC mammalian cancer cells, to induce NF-kappaB-dependent transcription and CC to induce JNK/SAPK-dependent responses in mammalian cells.

XX SQ Sequence 249 AA;

Query Match 100.0%; Score 1268; DB 20; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.4e-119; Mismatches 0; Indels 0; Gaps 0;  
Matches 249; Conservative 0;

QY 1 MAARRSQRRRGRGEPGTALLVPLALGLGLALACGLGLLAVVSLGSRASLSAQEPAQEEL 60  
Db 1 MAARRSQRRRGRGEPGTALLVPLALGLGLALACGLGLLAVVSLGSRASLSAQEPAQEEL 60

QY 61 VAEEDQPSSELNPQTESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120  
61 VAEEDQPSSELNPQTESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120

QY 121 GAQAGVDGTVSGWEEARINSSPLRYNROI GEFIVTRAGLYLYLCVHFDEGKAVYLKLD 180  
121 GAQAGVDGTVSGWEEARINSSPLRYNROI GEFIVTRAGLYLYLCVHFDEGKAVYLKLD 180

QY 181 LLDVGVLAALRCLEEFSAATASSLGPPQLRLCQVSGLLALRPGSSLRITLTPWAHLKAAPFL 240  
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QY 241 TYFGLFQVH 249  
241 TYFGLFQVH 249

RESULT 2  
AAB07526  
ID AAB07526 standard; protein; 249 AA.  
AC AAB07526;  
DT 20-OCT-2000 (first entry)  
XX Amino acid sequence of a soluble recombinant human TWEAK protein.  
DE TWEAK protein; immunological disorder; immune response; inflammation;  
KW TWEAK blocking agent; autoimmune disease; organ transplant rejection;  
KW Graft-versus-Host disease; GVHD; lymphoid cell malignancy; shock; tumour.

XX Homo sapiens.  
PN WO200042073-A1.  
PD 20-JUL-2000.  
XX 14-JAN-2000; 2000WO-US01044.  
XX 15-JAN-1999; 99US-0116168.  
XX (BIOJ ) BIOGEN INC.  
XX Rennert P;  
PI WPI; 2000-476036/41.  
XX Preventing and treating immune responses using modulators, especially  
PT antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, useful for  
PT treating e.g. inflammation and graft versus host disease -  
PS Disclosure; Fig 1; 45pp; English.  
XX The present sequence represents a TWEAK protein. The specification

CC describes a method for preventing or treating an immunological  
CC disorder and/or inhibiting an immune response in an animal. The  
CC method comprises administering a TWEAK blocking agent. The method may  
CC be used for preventing and treating immune disorders associated with  
CC inappropriate expression and/or activity of TWEAK. These disorders  
CC include autoimmune diseases, acute and chronic inflammation, organ  
CC transplant rejection; Graft-versus-Host disease (GVHD), lymphoid cell  
CC malignancies, septic and other forms of shock, loss of immune  
CC responsiveness (as seen in human immunodeficiency virus (HIV)  
CC infections) and failure of the immune response to tumour growth.

XX SQ Sequence 249 AA;

Query Match 100.0%; Score 1268; DB 21; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.4e-119; Mismatches 0; Indels 0; Gaps 0;  
Matches 249; Conservative 0;

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Db 1 MAARRSQRRRGRGEPGTALLVPLALGLGLALACGLGLLAVVSLGSRASLSAQEPAQEEL 60

QY 61 VAEEDQPSSELNPQTESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120  
61 VAEEDQPSSELNPQTESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120

QY 121 GAQAGVDGTVSGWEEARINSSPLRYNROI GEFIVTRAGLYLYLCVHFDEGKAVYLKLD 180  
121 GAQAGVDGTVSGWEEARINSSPLRYNROI GEFIVTRAGLYLYLCVHFDEGKAVYLKLD 180

QY 181 LLDVGVLAALRCLEEFSAATASSLGPPQLRLCQVSGLLALRPGSSLRITLTPWAHLKAAPFL 240  
181 LLDVGVLAALRCLEEFSAATASSLGPPQLRLCQVSGLLALRPGSSLRITLTPWAHLKAAPFL 240

QY 241 TYFGLFQVH 249  
241 TYFGLFQVH 249

RESULT 3  
AAY95338  
ID AAY95338 standard; protein; 249 AA.  
AC AAY95338;  
DT 25-SEP-2000 (first entry)  
XX Human PRO207 antitumour protein.  
DE PRO207; human; antitumour; tumour; therapy; cytostatic;  
KW breast cancer; ovarian cancer; renal cancer; colorectal cancer;  
KW uterine cancer; prostate cancer; lung cancer; bladder cancer;  
KW central nervous system cancer; melanoma; leukaemia; neoplasm.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1..40  
FT /label= Signal\_peptide  
FT Protein 41..249  
FT /label= PRO207  
FT Modified-site 27..33  
FT /note= "N-myristoylation"  
FT Modified-site 29..35  
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FT 10..14  
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FT 97..101  
FT Modified-site /note= "amidation"  
FT 24..35  
FT Peptide /note= "prokaryotic membrane lipoprotein lipid"  
FT 24..35  
XX WO200037638-A2.  
PN 29-JUN-2000.  
XX 02-DEC-1999; 99WO-US28565.  
XX 22-DEC-1998; 98US-0113296.  
XX 08-MAR-1999; 99WO-US05028.  
XX 21-APR-1999; 99US-0130232.  
XX 28-APR-1999; 99US-0131445.  
XX 14-MAY-1999; 99US-0134287.  
XX 20-JUL-1999; 99US-0144758.  
XX 26-JUL-1999; 99US-0145698.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;  
XX Napier MA, Pitti RM, Wood WI;  
XX WPI; 2000-442668/38.  
XX N-PSDB; AAA49717.  
XX Novel composition to inhibit neoplastic cell growth or for treating  
XX tumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219,  
XX PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or  
XX PRO866 .  
XX Claim 19; Fig 4; 172pp; English.  
XX The present sequence is that of human antitumor protein PRO207,  
XX as deduced from a foetal kidney cDNA clone (see AAA49717). PRO207  
XX shows amino acid sequence identity to tumour necrosis factor family  
XX members, especially human lymphotxin-beta (23.4%) and human CD40  
XX ligand (19.8%). Mol.wt. is 27,216. A claimed method for inhibiting  
XX the growth of a tumour cell comprises exposing the tumor cell  
XX to PRO179, PRO207, PRO320, PRO219, PRO221, PRO224, PRO328, PRO301,  
XX PRO526, PRO362, PRO356, PRO509 or PRO866 (see AAY95337-49), their  
XX agonists or chimeric polypeptides incorporating them. The tumour  
XX is especially a cancer selected from breast, ovarian, renal,  
XX colorectal, uterine, prostate, lung, bladder and central nervous  
XX system cancer, melanoma and leukaemia. Methods for the recombinant  
XX expression of the antitumour proteins are also provided.  
XX Sequence 249 AA;  
XX Query Match 100.0%; Score 1268; DB 21; Length 249;  
XX Best Local Similarity 100.0%; Pred. No. 1.4e-119;  
XX Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAARRSORRRGREGPTALLVPLALGLGLALACGLALLAWSLGSSASLSAQEPAQEEL 60  
Db |||||  
Db 1 MAARRSORRRGREGPTALLVPLALGLGLALACGLALLAWSLGSSASLSAQEPAQEEL 60  
QY 61 VAEDQDPSELNPOTESQDPAPFLNLRVPRRSAPKGRKTRARRAIAHYVHPREGQD 120  
Db |||||  
Db 61 VAEDQDPSELNPOTESQDPAPFLNLRVPRRSAPKGRKTRARRAIAHYVHPREGQD 120  
QY 121 GAQAGVDGTVSGWEEARINSSPLRNQIGEFIVTRAGLYLYCQVHDEGKAVYLKLD 180  
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Db 121 GAQAGVDGTVSGWEEARINSSPLRNQIGEFIVTRAGLYLYCQVHDEGKAVYLKLD 180  
QY 181 LLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240  
|||  
Db 181 LLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240  
QY 241 TYEGLFQVH 249  
|||  
Db 241 TYEGLFQVH 249  
RESULT 4  
AAU86129 ID AAU86129 standard; Protein; 249 AA.  
XX AC AAU86129;  
XX 15-JUL-2002 (first entry)  
XX Human PRO207 polypeptide.  
XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
XX leukaemia; neuronal disorder; stromal disorder; blastocoeleic disorder;  
XX inflammatory disorder; immune disorder; angiogenic disorder;  
XX cytostatic; neuroprotective.  
XX Homo sapiens.  
XX WO200153486-A1.  
XX 26-JUL-2001.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 08-MAR-1999; 99WO-US05028.  
XX 11-MAR-1999; 99US-123972P.  
XX 11-MAY-1999; 99US-133459P.  
XX 02-JUN-1999; 99WO-US12252.  
XX 22-JUN-1999; 99US-140650P.  
XX 22-JUN-1999; 99US-140653P.  
XX 20-JUL-1999; 99US-144758P.  
XX 26-JUL-1999; 99US-145698P.  
XX 28-JUL-1999; 99US-146222P.  
XX 17-AUG-1999; 99US-149395P.  
XX 31-AUG-1999; 99US-151689P.  
XX 01-SEP-1999; 99WO-US20111.  
XX 15-SEP-1999; 99WO-US21090.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28301.  
XX 01-DEC-1999; 99WO-US28634.  
XX 05-JAN-2000; 2000WO-US00219.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;  
XX Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;  
XX Watanabe CK, Wood WI;  
XX WPI; 2002-205567/26.  
XX N-PSDB; ABK40255.  
XX Thirty five nucleic acids encoding PRO polypeptides, useful for  
XX treating benign or malignant tumours, leukaemias and lymphoid  
XX malignancies, inflammatory, angiogenic and immunologic disorders -  
XX Claim 61; Fig 4; 302pp; English.  
XX The present invention relates to the isolation of novel human PRO  
XX polypeptides and the polynucleotide sequences encoding them. The  
XX PRO polypeptides, agonists, antagonists or anti-PRO antibodies are  
XX useful for treating benign or malignant tumours (e.g. renal, kidney,  
XX bladder, breast, etc), leukaemias and lymphoid malignancies, other  
XX disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,

CC macrophagal, stromal and blastocoelic disorders, inflammatory, immune  
 CC and angiogenic disorders. The polynucleotide sequences are also  
 CC useful in gene therapy. AAU86128-AAU86162 represent the human PRO  
 CC polypeptides of the invention.

XX Sequence 249 AA;

Query Match 100.0%; Score 1268; DB 23; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-119;  
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAARRSRRRRGEGPTALLVPLALGLGALACLGILLAVVSLGSRASLSAQEPQAEEL 60

Db 1 MAARRSRRRRGEGPTALLVPLALGLGALACLGILLAVVSLGSRASLSAQEPQAEEL 60

Qy 61 VAEDQDPSELNPQTEESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGQD 120

Db 61 VAEDQDPSELNPQTEESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGQD 120

Qy 121 GAAQGVDTGTVSGWEARINSSPLRYNQIGEFIVTRAGLYLYCQVHFDGKAVYLKLD 180

Db 121 GAAQGVDTGTVSGWEARINSSPLRYNQIGEFIVTRAGLYLYCQVHFDGKAVYLKLD 180

Qy 181 LLVDGVLAALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAHLKAAPFL 240

Db 181 LLVDGVLAALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAHLKAAPFL 240

Qy 241 TYFGLFQVH 249

Db 241 TYFGLFQVH 249

RESULT 5

AAW47525  
 ID AAW47525 standard; \*Protein; 284 AA.

XX AC AAW47525;

XX DT 21-JUL-1998 (first entry)

XX Homo sapiens tumour necrosis factor related ligand (TREL).

XX TREL; tumour necrosis factor related ligand; tnfr, treatment;  
 KW cancer; autoimmune disease; immune system; stimulation; suppression;  
 KW graft rejection.

XX OS Homo sapiens.

XX WO9805783-A1.

XX 12-FEB-1998.

XX 07-AUG-1997; 97WO-US13945.

XX 18-MAR-1997; 97US-0040820.

XX 07-AUG-1996; 96US-0023541.

XX 18-OCT-1996; 96US-0028515.

XX (BIOJ ) BIOGEN INC.  
 XX (UYGE-) UNIV GENEVA FACULTY MEDICINE.

XX Browning JL, Chicheportiche Y;

XX WPI; 1998-145619/13.

XX N-PSDB; AAV18600.

XX Tumour necrosis factor related ligand - useful for, e.g. treating

XX cancer, auto-immune disease and immune responses to tissue grafts

XX Claim 12; Pages 50-51; 69pp; English.

XX The sequence is that of human tumour necrosis factor related

XX ligand (TREL). TREL or active fragments can be included with a

CC carrier in pharmaceutical compositions to treat cancer, autoimmune  
 CC diseases or immune responses to tissue grafts, or to stimulate or  
 CC suppress the immune system. It is useful to screen for TREL  
 CC receptors, by labelling with a detectable label and screening  
 CC compositions for binding. Agents interfering with TREL-receptor  
 CC binding can also be screened for, can then be administered,  
 CC optionally with interferon- gamma, to induce cell death or  
 CC treat, suppress or alter immune responses (especially involving human  
 CC adenocarcinoma cells) involving a signal pathway between TREL and its  
 CC receptor. It's coding sequence can be used in gene therapy for  
 CC TREL-related disorders in mammals (especially humans), e.g. tumours,  
 CC autoimmune and inflammatory diseases or inherited genetic disorders,  
 CC by introducing into cells, and expressing, therapeutically effective,  
 CC amounts of a vector, e.g. a virus comprising a gene encoding TREL.  
 CC It may also be of use in the preparation of probe probes for  
 CC screening natural/synthetic DNAs for TREL-encoding sequences  
 CC and for antisense therapy.

SQ Sequence 284 AA;

Query Match 100.0%; Score 1268; DB 19; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-119;  
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAARRSRRRRGEGPTALLVPLALGLGALACLGILLAVVSLGSRASLSAQEPQAEEL 60

Db 36 MAARRSRRRRGEGPTALLVPLALGLGALACLGILLAVVSLGSRASLSAQEPQAEEL 95

Qy 61 VAEDQDPSELNPQTEESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGQD 120

Db 96 VAEDQDPSELNPQTEESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGQD 155

Qy 121 GAAQGVDTGTVSGWEARINSSPLRYNQIGEFIVTRAGLYLYCQVHFDGKAVYLKLD 180

Db 156 GAAQGVDTGTVSGWEARINSSPLRYNQIGEFIVTRAGLYLYCQVHFDGKAVYLKLD 215

Qy 181 LLVDGVLAALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAHLKAAPFL 240

Db 216 LLVDGVLAALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAHLKAAPFL 275

Qy 241 TYFGLFQVH 249

Db 276 TYFGLFQVH 284

RESULT 6

AAW29745  
 ID AAW29745 standard; Protein; 249 AA.

XX AC AAW29745;

XX DT 27-OCT-1998 (first entry)

XX TNF related endothelium proliferative agent protein.

XX TNF; endothelium proliferative agent; TRPFA; wound healing; cancer;  
 KW tissue grafting; vascularisation; apoptosis; autoimmune; Birth control.

XX OS Homo sapiens.

XX WO9835061-A2.

XX 13-AUG-1998.

XX 12-FEB-1998; 98WO-US02859.

XX 10-FEB-1998; 98US-0021706.

XX 12-FEB-1997; 97US-0798692.

XX (ABBO ) ABBOTT LAB.

XX Wiley SR;

DR WPI: 1998-447255/38.  
 DR N-PSDB; AAV47613.  
 XX Detecting nucleic acid encoding TREPA - useful for diagnosis and  
 PT treatment of autoimmune disease, tumours and inflammation  
 XX  
 PS Claim 16; Page 123-4; 142pp; English.  
 XX  
 CC The TNF-related endothelium proliferative agent (TREPA), or its  
 CC activators or agonists, are used to treat a deficit of TREPA, e.g. to  
 CC promote wound healing or tissue grafting, by promoting vascularisation,  
 CC also to induce apoptosis for treating cancer and eliminating autoreactive  
 CC T cells, as an adjunct to cancer chemotherapy or antiviral treatment.  
 CC TREPA peptides can also be used to target cytotoxic agents or for  
 CC affinity isolation of the corresponding receptor, the nucleic acid for  
 CC which can be used to transform tumour cells to render them more  
 CC responsive to TREPA and to screen for TREPA mimics.  
 CC Ribozymes, antisense RNA, antibodies or peptides, are used to treat  
 CC TREPA-associated diseases, e.g. tumours and metastases (by inhibiting  
 CC vascularisation), inflammation or a wide range of autoimmune conditions,  
 CC conditions involving abnormal stimulation of epithelial cells (e.g.  
 CC atherosclerosis), for birth control (inhibiting ovulation and placental  
 CC formation) or other angiogenic conditions (e.g. ulcers).  
 CC  
 CC Sequence 249 AA;  
 Query Match 99.8%; Score 1265; DB 19; Length 249;  
 Best Local Similarity 99.6%; Pred. No. 2.8e-119;  
 Matches 248; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAARRSRRRRGEGPTALLVPLALGLGLALACGLGLLLAVVSLGSRASLSAQEPAGEEL 60  
 Db 1 MAARRSRRRRGEGPTALLVPLALGLGLALACGLGLLLAVVSLGSRASLSAQEPAGEEL 60  
 QY 61 VAEDDQPSSELPNQTESQDPAPFLNLRVPRRSAPKGRKTRARRAIAAHVEVHPRGQD 120  
 Db 61 VAEDDQPSSELPNQTESQDPAPFLNLRVPRRSAPKGRKTRARRAIAAHVEVHPRGQD 120  
 QY 121 GAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYLYLYCQVHFDGKAVYLKLD 180  
 Db 121 GAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYLYLYCQVHFDGKAVYLKLD 180  
 QY 181 LLVDGVLAALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240  
 Db 181 LLVDGVLAALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240  
 QY 241 TYFGLFQVH 249  
 Db 241 TYFGLFQVH 249  
 RESULT 7  
 AAE00891  
 ID AAE00891 standard; Protein; 249 AA.  
 XX  
 AC AAE00891;  
 XX  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Human TREPA (TNF related endothelium proliferative agent).  
 XX  
 KW Human; tumour necrosis factor; TNF; angiogenesis; wound healing;  
 KW TREPA; TNF related endothelium proliferative agent; tumour; metastasis;  
 KW grafting; relnary.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 98..249  
 FT /label= Extracellular\_domain  
 FT  
 PN US6207642-B1.  
 XX

PD 27-MAR-2001.  
 XX  
 XX 26-JUN-1998; 98US-0105343.  
 PF  
 XX 12-FEB-1997; 97US-0798692.  
 PR  
 XX 10-FEB-1998; 98US-0021706.  
 PR  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 XX Wiley SR;  
 PI  
 XX WPI; 2001-280760/29.  
 DR  
 XX N-PSDB; AAD04350.  
 DR  
 XX Inducing angiogenesis in mammal at desired sites for promoting wound  
 PT healing, by administering soluble fragment of extracellular domain of  
 PT tumor necrosis factor related endothelium proliferative agent protein  
 PT  
 XX Claim 1; Column 75-76; 53pp; English.  
 PS  
 CC The present invention relates to extracellular signal molecules,  
 CC particularly members of tumour necrosis factor (TNF) family molecules  
 CC designated as TREPA (TNF related endothelium proliferative agent).  
 CC Soluble biologically active TREPA are used to treat TREPA-associated  
 CC diseases, tumours or metastases. TREPA is used for inducing angiogenesis  
 CC in human for promoting wound healing and for vascularising grafted  
 CC tissue for successful grafting and to promote tissue grafts.  
 CC The present amino acid sequence is clone ID #690050 human TREPA..  
 CC  
 CC Sequence 249 AA;  
 Query Match 99.8%; Score 1265; DB 22; Length 249;  
 Best Local Similarity 99.6%; Pred. No. 2.8e-119;  
 Matches 248; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAARRSRRRRGEGPTALLVPLALGLGLALACGLGLLLAVVSLGSRASLSAQEPAGEEL 60  
 Db 1 MAARRSRRRRGEGPTALLVPLALGLGLALACGLGLLLAVVSLGSRASLSAQEPAGEEL 60  
 QY 61 VAEDDQPSSELPNQTESQDPAPFLNLRVPRRSAPKGRKTRARRAIAAHVEVHPRGQD 120  
 Db 61 VAEDDQPSSELPNQTESQDPAPFLNLRVPRRSAPKGRKTRARRAIAAHVEVHPRGQD 120  
 QY 121 GAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYLYLYCQVHFDGKAVYLKLD 180  
 Db 121 GAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYLYLYCQVHFDGKAVYLKLD 180  
 QY 181 LLVDGVLAALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240  
 Db 181 LLVDGVLAALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240  
 QY 241 TYFGLFQVH 249  
 Db 241 TYFGLFQVH 249  
 RESULT 8  
 AAU03499  
 ID AAU03499 standard; Protein; 273 AA.  
 XX  
 AC AAU03499;  
 XX  
 DT 26-SEP-2001 (first entry)  
 XX  
 DE TWEAK extracellular domain-containing fusion protein.  
 XX  
 KW TWEAK extracellular domain; tumour necrosis factor; TNF; angiogenesis;  
 KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;  
 KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;  
 KW rubecosis; uveitis; macular degeneration; arthritis; rheumatism;  
 KW corneal graft neovascularisation; psoriasis; metastatic condition;  
 KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;  
 KW

KW preneoplastic condition; myocardial angiogenesis; wound granulation;  
 KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;  
 KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;  
 KW peripheral atherosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAKR;  
 KW fusion protein.

XX Homo sapiens.

OS Synthetic.

XX WO200145730-A2.

XX 28-JUN-2001.

XX 19-DEC-2000; 2000WO-US34755.

XX 20-DEC-1999; 99US-0172878.

XX 10-MAY-2000; 2000US-0203347.

XX (IMMUNEX CORP.

XX Wiley SR;

XX WPI; 2001-417975/44.

XX N-PSDB; AAS03964.

XX Modulating angiogenesis in a mammal for treating diseases mediated by

XX angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac or

XX peripheral tissue, by administering antagonist or agonist of TWEAK

XX receptor -

XX Example 1; Page 41; 46pp; English.

XX The sequence represents a fusion protein encoded by the

XX expression vector pDC409-LZ-TWEAK. The fusion protein comprises a

XX growth hormone leader, a leucine zipper multimerisation domain, and

XX the extracellular domain of human TWEAK. The fusion protein was

XX used in the isolation of human TWEAK receptor (TWEAKR)-expressing

XX clones from a COS cell human cDNA library. The TWEAK protein is

XX a member of the tumour necrosis factor (TNF) family and induces

XX angiogenesis. TWEAKR may therefore be used to screen for and

XX develop TWEAKR agonists and antagonists for the modulation of

XX angiogenesis, to be used in the treatment and diagnosis of human disease.

XX The disorders mediated by angiogenesis include ocular disorders

XX characterised by ocular neovascularisation such as diabetic retinopathy,

XX neovascular glaucoma, retinoblastoma, retinopathy of prematurity,

XX retrolental fibroplasia, rubecosis, uveitis, macular degeneration and

XX corneal graft neovascularisation, and inflammatory diseases such as

XX arthritis, rheumatism and psoriasis. Other treatable diseases include

XX malignant and metastatic conditions such as sarcomas and carcinomas,

XX benign tumours and preneoplastic conditions, myocardial angiogenesis,

XX haemophilic joints, scleroderma, vascular adhesions, atherosclerotic

XX plaque neovascularisation, telangiectasia, wound granulation, coronary

XX atherosclerosis, peripheral atherosclerosis and ischaemia.

XX Sequence 273 AA;

XX Query Match 84.1%; Score 1066; DB 22; Length 273;

XX Best Local Similarity 100.0%; Pred. No. 4e-99;

XX Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 SLGSRASLSAQEPQAEELVAEEDQDPSELNQTETESQDPAPFLNRLVPRPSAPKGRKTR 102

DB 67 SLGSRASLSAQEPQAEELVAEEDQDPSELNQTETESQDPAPFLNRLVPRPSAPKGRKTR 126

QY 103 ARRAIAHYEHPHPPGQAGVGDGTSGWEEARINSSPLRYNRQIGEIFVTRAGLYY 162

DB 127 ARRAIAHYEHPHPPGQAGVGDGTSGWEEARINSSPLRYNRQIGEIFVTRAGLYY 186

QY 163 LYCQVHFDEGKAVYKLLDLLVDGVLALRCLEFFSATAASSLGPQLRQCQVSGLLALRPGS 222

DB 167 LYCQVHFDEGKAVYKLLDLLVDGVLALRCLEFFSATAASSLGPQLRQCQVSGLLALRPGS 246

QY 223 SLRIRTLPAHLKAAPFLTYFGLFQVH 249

DB 247 SLRIRTLPAHLKAAPFLTYFGLFQVH 273

RESULT 9

AAW93590

ID AAW93590 standard; Protein; 208 AA.

XX AAW93590;

AC AAW93590;

XX 18-JUN-1999 (first entry)

DT Human TNRL3 protein.

XX Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;

XX developmental abnormality; gestational abnormality; prostate cancer;

XX APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;

XX cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;

XX apoptosis; human.

XX Homo sapiens.

OS WO9911791-A2.

XX 11-MAR-1999.

PD 04-SEP-1998; 98WO-US18393.

XX 05-SEP-1997; 97US-0924634.

XX (UNIW ) UNIV WASHINGTON.

XX Chaudhary PM;

PI WPI; 1999-205191/17.

XX N-PSDB; AAX23424.

XX New Tumor Necrosis Factor family receptor polypeptides and ligands -

XX useful for diagnosis and treatment of prostate cancer and

XX developmental or gestational abnormalities

XX Claim 40; Fig 13A; 156pp; English.

XX This invention describes isolated Tumor Necrosis Factor (TNF) family

XX receptor polypeptides: APO4, APO6, APO8 and APO9 or their active

XX fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or

XX their active fragments. APO4 is useful for diagnosing prostate cancer

XX by determining levels of APO4 in an individual. Prostate cancer can also

XX be treated using APO4 selective binding agents linked to a therapeutic

XX moiety. APO4 polypeptides are also useful for identifying selective

XX binding agents, useful in diagnosis/treatment of disease by binding of

XX agents to the polypeptide/active fragment which is extracellular. Or

XX expressed on the cell surface. The binding is preferably performed in

XX vivo. APO4 polypeptides/ active fragments are also useful for screening

XX for agonists and antagonists by binding and observing the change in APO4

XX activity. Effective pharmacological agents useful in diagnosis or

XX treatment of disease are also identified using APO4 polypeptides/active

XX fragments and APO4 signal transducer molecules that specifically interact

XX with a cytoplasmic domain of APO4 and detecting a change in level of APO4

XX activity. The method is performed in vivo or in vitro. APO polypeptides

XX are all useful as immunogens for preparing antibodies. APO4 is also

XX useful for diagnosis/treatment of developmental or gestational

XX abnormalities. APO8 was transfected to human breast carcinoma cell line

XX MCF-7, and induced apoptosis.

XX Sequence 208 AA;

XX Query Match 83.8%; Score 1062; DB 20; Length 208;

XX Best Local Similarity 99.5%; Pred. No. 6.8e-99;

XX Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 42 VSLGSRASLSAQEPQAEELVAEEDQDPSELNQTETESQDPAPFLNRLVPRPSAPKGRKT 101



Db 1 VLSGRASLSAQEAQELVAEDDPSSELNPQTEESODPAPFLNRLVPRRSAPKGRKT 60  
 QY 102 RARRAIAAHYEVHPRPGDGAQAGVDGTVSGWEARINSSSPLRYNRQIGEFIVTRAGLY 161  
 Db 61 RARRAIAAHYEVHPRPGDGAQAGVDGTVSGWEARINSSSPLRYNRQIGEFIVTRAGLY 120  
 QY 162 YLYCQVHFDEGKAVYKLDLLVDGVLALRCLEEPSATASLSGLPOLRLCQVSGLLALRPG 221  
 Db 121 YLYCQVHFDEGKAVYKLDLLVDGVLALRCLEEPSATASLSGLPOLRLCQVSGLLALRPG 180  
 QY 222 SSLRIRTLPAWHLKAAPLTYFGLFOVH 249  
 Db 181 SSLRIRTLPAWHLKAAPLTYFGLFOVH 208  
 RESULT 10  
 AAW47524  
 ID AAW47524 standard; Protein; 225 AA.  
 YV AAW47524;  
 L. 21-JUL-1998 (first entry)  
 XX Mus musculus tumour necrosis factor related ligand (TRELL).  
 DE TRELL; tumour necrosis factor related ligand; tnf; treatment;  
 KW cancer; autoimmune disease; immune system; stimulation; suppression;  
 KW graft rejection.  
 XX Mus musculus.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..21  
 FT /note= "hydrophobic, transmembrane domain"  
 XX  
 PN WO9805783-A1.  
 XX 12-FEB-1998.  
 PD  
 XX  
 PF 07-AUG-1997; 97WO-US13945.  
 XX  
 XX 18-MAR-1997; 97US-0040820.  
 PR 07-AUG-1996; 96US-0023541.  
 PR 18-OCT-1996; 96US-0028515.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 PA (UYGE-) UNIV GENEVA FACULTY MEDICINE.  
 Browning JL, Chicheportiche Y;  
 WPI; 1998-145619/13.  
 DR N-PSDB; AAV18599.  
 XX  
 XX Tumour necrosis factor related ligand - useful for, e.g. treating  
 PT cancer, auto-immune disease and immune responses to tissue grafts  
 XX  
 PS Claim 12; Pages 48-50; 69pp; English.  
 XX  
 XX The sequence is that of mouse tumour necrosis factor related  
 CC ligand (TRELL). TRELL or active fragments can be included with a  
 CC carrier in pharmaceutical compositions to treat cancer, autoimmune  
 CC diseases or immune responses to tissue grafts, or to stimulate or  
 CC suppress the immune system. It is useful to screen for TRELL  
 CC receptors, by labelling with a detectable label and screening  
 CC compositions for binding. Agents interfering with TRELL-receptor  
 CC binding can also be screened for, can then be administered,  
 CC optionally with interferon- gamma, to induce cell death or  
 CC treat, suppress or alter immune responses (especially involving human  
 CC adenocarcinoma cells) involving a signal pathway between TRELL and its  
 CC receptor. It's coding sequence can be used in gene therapy for  
 CC TRELL-related disorders in mammals (especially humans), e.g. tumours,  
 CC autoimmune and inflammatory diseases or inherited genetic disorders,  
 CC by introducing into cells, and expressing, therapeutically effective

CC amounts of a vector, e.g. a virus comprising a gene encoding TRELL.  
 CC It may also be of use in the preparation of prepare probes for  
 CC screening natural/synthetic DNAs for TRELL-encoding sequences  
 CC and for antisense therapy.  
 XX  
 SQ Sequence 225 AA;  
 Query Match 80.4%; Score 1020; DB 19; Length 225;  
 Best Local Similarity 88.8%; Pred. No. 1.3e-94;  
 Matches 199; Conservative 9; Mismatches 16; Indels 0; Gaps 0;  
 QY 26 LSLGLALACLGILLAVVSLGSRASLSAQEAQELVAEDDPSSELNPQTEESODPAPFL 85  
 Db 2 LSLGLALACLGILLAVVSLGSRASLSAQEAQELVAEDDPSSELNPQTEESODPAPFL 61  
 QY 86 NRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGDGAQAGVDGTVSGWEARINSSSPLR 145  
 Db 62 EQLVPRRSAPKGRKTRARRAIAAHYEVHPRPGDGAQAGVDGTVSGWEARINSSSPLR 121  
 QY 146 YNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYKLDLLVDGVLALRCLEEPSATASLSGLP 205  
 Db 122 YDRQIGEFIVTRAGLYYLYCQVHFDEGKAVYKLDLLVDGVLALRCLEEPSATASLSGLP 181  
 QY 206 QLRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPLTYFGLFOVH 249  
 Db 182 QLRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPLTYFGLFOVH 225  
 RESULT 11  
 AAB07527  
 ID AAB07527 standard; protein; 225 AA.  
 AC AAB07527;  
 XX  
 DT 20-OCT-2000 (first entry)  
 XX  
 DE Amino acid sequence of a soluble recombinant murine TWEAK protein.  
 XX TWEAK protein; immunological disorder; immune response; inflammation;  
 KW TWEAK blocking agent; autoimmune disease; organ transplant rejection;  
 KW Graft-versus-Host disease; GVHD; lymphoid cell malignancy; shock; tumour.  
 XX  
 OS Mus sp.  
 XX WO2000042073-A1.  
 PN  
 XX 20-JUL-2000.  
 PD  
 XX 14-JAN-2000; 2000WO-US01044.  
 PF  
 XX 15-JAN-1999; 99US-0116168.  
 PR  
 XX (BIOJ ) BIOGEN INC.  
 PA  
 XX Rennert P;  
 PI  
 XX WPI; 2000-476036/41.  
 DR  
 XX Preventing and treating immune responses using modulators, especially  
 PT antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, useful for  
 PT treating e.g. inflammation and graft versus host disease -  
 XX  
 PS Disclosure; Fig 1; 45pp; English.  
 XX  
 CC The present sequence represents a TWEAK protein. The specification  
 CC describes a method for preventing or treating an immunological  
 CC disorder and/or inhibiting an immune response in an animal. The  
 CC method comprises administering a TWEAK blocking agent. The method may  
 CC be used for preventing and treating immune disorders associated with  
 CC inappropriate expression and/or activity of TWEAK. These disorders  
 CC include autoimmune diseases, acute and chronic inflammation, organ  
 CC transplant rejection, Graft-versus-Host disease (GVHD), lymphoid cell  
 CC malignancies, septic and other forms of shock, loss of immune

CC responsiveness (as seen in human immunodeficiency virus (HIV)  
CC infections) and failure of the immune response to tumour growth.  
XX  
SQ Sequence 225 AA; 80.4%; Score 1020; DB 21; Length 225;  
Query Match 88.8%; Pred. No. 1.3e-94;  
Best Local Similarity 9; Mismatches 16; Indels 0; Gaps 0;  
Matches 199; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 26 LGLGLALACLGILLAVSLGSRASLSAQEPQAEELVAEDQDPSELNPQTEESQDPAPFL 85  
DB 2 LSLGLALACLGILLVVSLSGWATLSAQEPQAEELVAEDQDPSELNPQTEESQDPVFL 61  
QY 86 NRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGDGAQAGVDGTVSGWEARINSSSPLR 145  
DB 62 EQLVPRRSAPKGRKTRARRAIAAHYEVHPRPGDGAQAGVDGTVSGWEETKINSSSPLR 121  
QY 146 YNRQIGEFIVTRAGLYLYCOVHDEGKAVYKLDLLVDGVLALRCLEEPSATASSILGP 205  
DB 122 YDRQIGEFIVTRAGLYLYCOVHDEGKAVYKLDLLVNGVLALRCLEEPSATASSSGP 181  
206 QLRICQVSGLLALPGSSLRIRTLPAWHLKAAPFLTYFGLFQVH 249  
DB 182 QLRICQVSGLLALPGSSLRIRTLPAWHLKAAPFLTYFGLFQVH 225

RESULT 12  
AAW93591  
ID AAW93591 standard; Protein; 211 AA.  
XX  
AC AAW93591;  
XX  
DT 18-JUN-1999 (first entry)  
XX  
DE Mouse TNRL3 protein.  
XX  
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;  
KW developmental abnormality; gestational abnormality; prostate cancer;  
KW APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;  
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;  
KW apoptosis; mouse.  
XX  
OS Mus sp.  
XX  
PN WO9911791-A2.  
XX  
PD 11-MAR-1999.  
XX  
XY 04-SEP-1998; 98WO-US18393.  
XX  
XX 05-SEP-1997; 97US-0924634.  
XX  
XX (UNIW ) UNIV WASHINGTON.  
XX  
XX Chaudhary PM;  
XX  
XX WPI; 1999-205191/17.  
XX  
XX N-PSDB; AAX23425.  
XX  
PT New Tumour Necrosis Factor family receptor polypeptides and ligands -  
PT useful for diagnosis and treatment of prostate cancer and  
PT developmental or gestational abnormalities  
XX  
XX Claim 40; Fig 13B; 156pp; English.  
XX  
XX This invention describes isolated Tumour Necrosis Factor (TNF) family  
XX receptor polypeptides: APO4, APO6, APO8 and APO9 or their active  
XX fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or  
XX their active fragments. APO4 is useful for diagnosing prostate cancer  
XX by determining levels of APO4 in an individual. Prostate cancer can also  
XX be treated using APO4 selective binding agents linked to a therapeutic  
XX moiety. APO4 polypeptides are also useful for identifying selective  
XX binding agents, useful in diagnosis/treatment of disease by binding of

CC agents to the polypeptide/active fragment which is extracellular, or  
CC expressed on the cell surface. The binding is preferably performed in  
CC vivo. APO4 polypeptides/ active fragments are also useful for screening  
CC for agonists and antagonists by binding and observing the change in APO4  
CC activity. Effective pharmacological agents useful in diagnosis or  
CC treatment of disease are also identified using APO4 polypeptides/active  
CC fragments and APO4 signal transducer molecules that specifically interact  
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4  
CC activity. The method is performed in vivo or in vitro. APO polypeptides  
CC are all useful as immunogens for preparing antibodies. APO4 is also  
CC useful for diagnosis/treatment of developmental or gestational  
CC abnormalities. APO8 was transfected to human breast carcinoma cell line  
CC MCF-7, and induced apoptosis.  
XX  
SQ Sequence 211 AA;  
Query Match 76.3%; Score 968; DB 20; Length 211;  
Best Local Similarity 89.1%; Pred. No. 2.1e-89;  
Matches 188; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 39 LAVVSLGSRASLSAQEPQAEELVAEDQDPSELNPQTEESQDPAPFLNRLVPRRSAPKG 98  
DB 1 LVVSLGSRASLSAQEPQAEELVAEDQDPSELNPQTEESQDPVFLNRLVPRRSAPKG 60  
QY 99 RKTARPAIAAHYEVHPRPGDGAQAGVDGTVSGWEARINSSSPLRYNQIGEFIVTRA 158  
DB 61 RKARPRRAIAAHYEVHPRPGDGAQAGVDGTVSGWEETKINSSSPLRYQIGEFIVTRA 120  
QY 159 GLVLYLCQVHFDGKAVYKLDLLVDGVLALRCLEEPSATASSILGPQLRLCQVSGLLAL 218  
DB 121 GLVLYLCQVHFDGKAVYKLDLLVNGVLALRCLEEPSATASSILGPQLRLCQVSGLLAL 180  
QY 219 RPSGLRIRTLPAWHLKAAPFLTYFGLFQVH 249  
DB 181 RPSGLRIRTLPAWHLKAAPFLTYFGLFQVH 211

RESULT 13  
AAW29746  
ID AAW29746 standard; Protein; 189 AA.  
XX  
AC AAW29746;  
XX  
DT 27-OCT-1998 (first entry)  
XX  
DE TNF related endothelium proliferative agent protein 2.  
XX  
KW TNF; endothelium proliferative agent; TREPA; wound healing; cancer;  
KW tissue grafting; vascularisation; apoptosis; autoimmune; birth control.  
XX  
OS Homo sapiens.  
XX  
XX WO9835061-A2.  
XX  
XX 13-AUG-1998.  
XX  
XX 12-FEB-1998; 98WO-US02859.  
XX  
XX 10-FEB-1998; 98US-0021706.  
XX  
XX 12-FEB-1997; 97US-0798692.  
XX  
XX (ABBO ) ABBOTT LAB.  
XX  
XX Wiley SR;  
XX  
XX WPI; 1998-447255/38.  
XX  
XX Detecting nucleic acid encoding TREPA - useful for diagnosis and  
XX treatment of autoimmune disease, tumours and inflammation  
XX  
XX Claim 16; Page 125-6; 142pp; English.  
XX  
XX The TNF-related endothelium proliferative agent (TREPA), or its

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2003, 08:38:14 ; Search time 14 Seconds  
(without alignments)  
523.308 Million cell updates/sec

Title: US-09-905-810-2

Perfect score: 1268  
Sequence: 1 MAARRSQRGRGEGFTAL.....PWAHLKAAPFLTYGLFQVH 249

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

rchred: 262574 seqs, 29422922 residues

al number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: +  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1265	99.8	249	4	US-09-105-343A-2
2	792	62.5	189	4	US-09-105-343A-3
3	761	60.0	146	4	US-09-105-343A-6
4	95.5	7.5	254	1	US-08-236-918A-4
5	95.5	7.5	254	4	US-09-150-864A-4
6	91.5	7.2	240	4	US-08-913-014A-1
7	91.5	7.2	240	4	US-09-072-993C-4
8	90	7.1	659	4	US-09-562-737-11
9	90	7.1	660	3	US-08-819-177-1
10	89	7.0	256	4	US-09-320-424-13
11	88.5	7.0	659	4	US-09-562-737-18
12	87	6.9	253	4	US-09-320-424-11
13	87	6.9	253	1	US-08-670-354-6
14	87	6.9	231	4	US-09-320-424-6
15	87	6.9	231	5	PCT-US96-10895-6
16	86	6.8	1323	1	US-08-026-138B-4
17	85	6.7	294	3	US-08-996-139-11
18	85	6.7	294	4	US-08-995-659-11
19	85	6.7	294	4	US-09-215-649A-11
20	85	6.7	294	4	US-09-577-780-11
21	83.5	6.6	247	4	US-09-157-864-4
22	83.5	6.6	885	1	US-08-042-747A-8
23	83.5	6.6	885	3	US-08-804-439A-23
24	83.5	6.6	885	3	US-08-720-229-23
25	82	6.5	248	3	US-08-341-018-52
26	82	6.5	248	4	US-08-470-335-210
27	82	6.5	248	4	US-08-470-339-210

28	82	6.5	248	4	US-08-467-602-207	Sequence 207, App
29	82	6.5	248	4	US-08-467-602-404	Sequence 404, App
30	82	6.5	349	4	US-08-470-335-188	Sequence 188, App
31	82	6.5	382	4	US-08-467-602-382	Sequence 382, App
32	82	6.5	405	4	US-08-467-602-384	Sequence 384, App
33	82	6.5	411	4	US-08-470-339-189	Sequence 189, App
34	82	6.5	414	4	US-08-470-339-188	Sequence 188, App
35	82	6.5	422	1	US-08-036-555B-170	Sequence 170, App
36	82	6.5	422	1	US-08-469-569-170	Sequence 170, App
37	82	6.5	422	1	US-08-428-926-3	Sequence 3, Appli
38	82	6.5	422	1	US-08-249-322A-170	Sequence 170, App
39	82	6.5	422	1	US-08-428-927-3	Sequence 3, Appli
40	82	6.5	422	1	US-08-428-298-3	Sequence 3, Appli
41	82	6.5	422	1	US-08-339-517-3	Sequence 3, Appli
42	82	6.5	422	1	US-08-469-526A-170	Sequence 170, App
43	82	6.5	422	2	US-08-734-591A-170	Sequence 170, App
44	82	6.5	422	2	US-08-469-660-170	Sequence 170, App
45	82	6.5	422	3	US-08-341-018-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1  
US-09-105-343A-2  
; Sequence 2, Application US/09105343A  
; Patent No. 6207642  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, S. R.  
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-6050  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/105.343A  
; FILING DATE: 12-FEB-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/02859  
; FILING DATE: 12-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BECKER, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6048.US.P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847-935-1729  
; TELEFAX: 847-938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 249 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: NO. 6207642e  
; US-09-105-343A-2

Query Match 99.8%; Score 1265; DB 4; Length 249;  
Best Local Similarity 99.6%; Pred. No. 4.3e-120;  
Matches 248; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAARRSQRGRGEGFTALVPLALGLALACLLGLLWVSLGSRASLSAQEPAQEL 60

Db 1 MAARRSKRRGREGPTALLVPLALGLGLALACLLGLLLAVSLGSRASLSAQEPAGEEL 60  
QY 61 VAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120  
Db 61 VAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120  
QY 121 GAQAGVDGTVSGWEARINSSPLRYNRQIGFEFIVTRAGLYLYLCQVHDEGKAVYIKLD 180  
Db 121 GAQAGVDGTVSGWEARINSSPLRYNRQIGFEFIVTRAGLYLYLCQVHDEGKAVYIKLD 180  
QY 181 LLDVGVLLALRCLEFSATASSLGQPLRLCOVSGLLALRPGLSSLRIRTLPAWHLKAAPFL 240  
Db 181 LLDVGVLLALRCLEFSATASSLGQPLRLCOVSGLLALRPGLSSLRIRTLPAWHLKAAPFL 240  
QY 241 TYFGLFQVH 249  
Db 241 TYFGLFQVH 249  
RESULT 2  
US-09-105-343A-3  
; Sequence 3, Application US/09105343A  
; Patent No. 6207642  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, S.R.  
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-6050  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/105,343A  
; FILING DATE: 12-FEB-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/02859  
; FILING DATE: 12-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BECKER, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6048.US.P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847-935-1729  
; TELEFAX: 847-938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 189 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6207642e  
US-09-105-343A-3  
Query Match 62.5%; Score 792; DB 4; Length 189;  
Best Local Similarity 99.3%; Pred. No. 1.9e-72;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 97 KGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEARINSSPLRYNRQIGFEFIVT 156  
Db 37 KGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEARINSSPLRYNRQIGFEFIVT 96

QY 157 RAGLYLYLCQVHDEGKAVYIKLDLLVDGVLLALRCLEFSATASSLGQPLRLCOVSGLL 216  
Db 97 RAGLYLYLCQVHDEGKAVYIKLDLLVDGVLLALRCLEFSATASSLGQPLRLCOVSGLL 156  
QY 217 ALRPGSSLRIRTLPAWHLKAAPFLTYFGLFQVH 249  
Db 157 ALRPGSSLRIRTLPAWHLKAAPFLTYFGLFQVH 189  
RESULT 3  
US-09-105-343A-6  
; Sequence 6, Application US/09105343A  
; Patent No. 6207642  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, S.R.  
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-6050  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/105,343A  
; FILING DATE: 12-FEB-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/02859  
; FILING DATE: 12-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BECKER, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6048.US.P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847-935-1729  
; TELEFAX: 847-938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 146 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6207642e  
US-09-105-343A-6  
Query Match 60.0%; Score 761; DB 4; Length 146;  
Best Local Similarity 100.0%; Pred. No. 1.8e-69;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 104 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEARINSSPLRYNRQIGFEFIVTRAGLYYL 163  
Db 1 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEARINSSPLRYNRQIGFEFIVTRAGLYYL 60  
QY 164 YCQVHDEGKAVYIKLDLLVDGVLLALRCLEFSATASSLGQPLRLCOVSGLLALRPGSS 223  
Db 61 YCQVHDEGKAVYIKLDLLVDGVLLALRCLEFSATASSLGQPLRLCOVSGLLALRPGSS 120  
QY 224 LRIRTLPAWHLKAAPFLTYFGLFQVH 249  
Db 121 LRIRTLPAWHLKAAPFLTYFGLFQVH 146  
RESULT 4  
US-08-236-918A-4

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Query Match      7.5%; Score 95.5; DB 1; Length 254;
Best Local Similarity 25.7%; Pred. No. 0.075;
Matches 66; Conservative 31; Mismatches 87; Indels 73; Gaps 11;

19 ALLVPLALGLGLACLGCLLLAVSL-GSRASL-SAQEPAQEELVAEDQDPSELNPQTE 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
30 ALVAGLLULLLLAAACAVFLACPWAVSGARASPGSAASPLRE-----GPELSP--- 78
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
77 ESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGDGAQAGVDGTSGWEE- 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
79 --DDPAGLLDI-----RGMFAQLVAQNVL-----IDGPLSWYSDP 113
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 136 --ARINSSPLRYNRQICEFIVTRAGLYLYLCQVHDEGKAVYLLKDLLVDG-----VL 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 114 GLAGVSLTGGLSYKEDTKELVAKAGVYVFFQ-----LELRVAVAGEGSGVSL 163
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 188 ALRCLEBFSSTAASLGQRLCQVSG-----LLALRPGSSLRTRTUPWAHLK 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 164 ALHLQPLRSAAGAALALTVDLPASSEARNSAFGQGRLLHLHGAGQLRGVLLHTEARAR 223
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QY 236 AAPFL-----TYFGLFOV 248
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 HAWOLQTGATVLGLFRV 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
US-09-150-864A-4
; Sequence 4, Application US/09150864A
; Patent No. 6355779
; GENERAL INFORMATION:

```

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; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
; TITLE OF INVENTION: That Binds Theteto
; FILE REFERENCE: 2801-8
; CURRENT APPLICATION NUMBER: US/09/150,864A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/060,843
; PRIOR FILING DATE: 1993-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens(clone: human4-1BB-L(7A))
US-09-150-864A-4

Query Match 7.5%; Score 95.5; DB 4; Length 254;
Best Local Similarity 25.7%; Pred. No. 0.075;
Matches 66; Conservative 31; Mismatches 87; Indels 73; Gaps

QY 19 ALLVPLALGLGLALACGLLLAVSL-GSRASL-SAQEPAQEELVAEEDQDPSELNPQTE 76
Db 30 ALVAGLLLLLLLAACVFLACPAWVGARASPGSAASPRLE-----GPELSP--- 78

QY 77 ESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPFGQDCAQAGVDGTVSGWEE- 135
Db 79 --DDPAGLLDL-----RQGMFAQLVAQNVL-----IDGPLSWYSDP 113

QY 136 --ARINSSPLRYNRQIGFIVTRAGLYLYVCQHFDEGKAVYLLKDLLVDG-----VL 187
Db 114 GLAGVSLUTGGLSYKEDTKELVWAKAGVYVFFQ-----LELRVWAGEGSGVSL 163

QY 188 ALRCLSEFATASSIGPOLRLCQVSG-----LLALRPGSSLRIRTLPPWAHLK 235
Db 164 ALHLQPLRSAAGAAALUATVLPASSSEARNSAFGQGRLLHLHSAGQRLGVHLHTEAPAR 223

QY 236 AAPFL---TYFGLFQV 248
Db 224 HAWQLTQGTATVLGLFRV 240

RESULT 6
US-08-913-014A-1
; Sequence 1. Application US/08913014A
; Patent No. 6235878
; GENERAL INFORMATION:
; APPLICANT: Nishi, Kazunori
; APPLICANT: Hikichi, Yukiko
; APPLICANT: Shintani, Yasushi
; TITLE OF INVENTION: NOVEL FAS LIGAND-LIKE PROTEIN, ITS
; TITLE OF INVENTION: PRODUCTION AND USE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin, Esq.
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & USHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston,
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,014A
; FILING DATE: 04-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/02480

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Db 144 -ISKDGKTLG--QKIESWESSRKGHSFLNHVLPFNGELVIEQGLYIYSQTYF 169

RESULT 14

US-09-320-424-6

; Sequence 6, Application US/09320424

; Patent No. 6284236

; GENERAL INFORMATION:

; APPLICANT: Wiley, Steven R.

; APPLICANT: Goodwin, Raymond G.

; TITLE OF INVENTION: Cytokine that Induces Apoptosis

; FILE REFERENCE: 2835-E

; CURRENT APPLICATION NUMBER: US/09/320,424

; CURRENT FILING DATE: 1999-05-26

; EARLIER APPLICATION NUMBER: 09/190,046

; EARLIER FILING DATE: 1998-11-10

; EARLIER APPLICATION NUMBER: 09/048,641

; EARLIER FILING DATE: 1998-03-26

; EARLIER APPLICATION NUMBER: 08/670,354

; EARLIER FILING DATE: 1996-06-25

; EARLIER APPLICATION NUMBER: 08/548,368

; EARLIER FILING DATE: 1995-11-01

; EARLIER APPLICATION NUMBER: 08/496,632

; EARLIER FILING DATE: 1995-06-29

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 291

; TYPE: PRT

; ORGANISM: murine

US-09-320-424-6

Query Match 6.9%; Score 87; DB 4; Length 291;

Best Local Similarity 27.2%; Pred. No. 0.65;

Matches 31; Conservative 16; Mismatches 53; Indels 14;

QY 58 EELVABEDQDPSELNQTOTESQDPAPFLNLVLPFRSAP--KGRKTRARRAIAAHVEV

Db 93 EEVTLRTFQDTISTVPEKQLSTPPLP---RGRGPKQVAAHITGITRRNSALIP----

QY 116 RPQDGAQAGVDGTGSGWEARINSSPLEYRNQIGEFIVTRAGLYLYCOVHF 169

Db 144 -ISKDGKTLG--QKIESWESSRKGHSFLNHVLPFNGELVIEQGLYIYSQTYF 169

RESULT 15

PCI-US96-10895-6

; Sequence 6, Application PC/TUS9610895

; GENERAL INFORMATION:

; APPLICANT: Immunex Corporation.

; TITLE OF INVENTION: Cytokine That Induces Apoptosis

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple 7.5.2

; SOFTWARE: Microsoft Word, Version 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCI/US96/10895

; FILING DATE: 25-JUN-1996

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/496,632

; FILING DATE: 29-JUN-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:



```

; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756922
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10895-6

      6.9%; Score 87; DB 5; Length 291;
      27.2%; Pred. No. 0.65;
      31; Conservative 16; Mismatches 53; Indels 14; Gaps 4;

Qy 58 BELVAEEEDDPSELNPQTEESQDPAPFLNRLVPRRSAP--KGRKTRARRAIAAHYEVHP 115
Db 93 EEVTLRTFDITSTVPEKQLSTPPLP---RGGRPQKVAAHITGTRRSNSALIP----- 143
Qy 116 RPDGAGAGVDGTSGWGEARINSSPLRYNQIGEFIVTRAGLYLYCQVHF 169
Db 144 -ISKDKTLG--QKTESWESSRKHSFLNHVLFNGELVIEQEGLYIYSQTYF 194
```

Search completed: April 12, 2003, 08:39:40  
Job time : 16 secs







Search completed: April 12, 2003, 08:40:10  
Job time : 26 secs

GenCore version 5.1.4\_p5.4578  
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OM protein - protein search, using sw model

Run on: April 12, 2003, 08:38:14 ; Search time 12 Seconds  
(without alignments)  
860.634 Million cell updates/sec

Title: US-09-905-810-2

Perfect score: 1268

Sequence: 1 MAARRSRRRRGRGEPGTA.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	100.0	249	1 TN12_HUMAN	O43508 homo sapien
2	1020	80.4	225	1 TN12_MOUSE	O34907 mus musculus
3	109.5	8.6	272	1 TNF5_CHICK	O91808 gallus gall
4	108.5	8.6	260	1 TNF5_CANFA	O97626 canis famil
5	95.5	7.5	201	1 TNF5_MACEU	O9xt48 macropus eu
6	95.5	7.5	254	1 TNF9_HUMAN	P41273 homo sapien
7	91.5	7.2	240	1 TN14_HUMAN	O43557 homo sapien
8	90	7.1	441	1 CG22_ANTMA	F34801 antirrhinum
9	90	7.1	707	1 JIPI_MOUSE	O9wv19 mus musculus
10	87	6.9	197	1 TNFB_RABIT	F10154 oryctolagus
11	87	6.9	204	1 TNFB_BOVIN	O06600 bos taurus
12	87	6.9	291	1 TN10_MOUSE	P50592 mus musculus
13	87	6.9	310	1 Y497_MYCTU	O11162 mycobacteri
14	86.5	6.8	250	1 TNFC_MACEU	O3xt47 macropus eu
15	86	6.8	139	1 YQFB_BACSU	P54467 bacillus su
16	86	6.8	205	1 TNFB_MARMO	O9jmo9 marmota mon
17	85	6.7	372	1 LMXB_MOUSE	O88609 mus musculus
18	85	6.7	379	1 LMXB_HUMAN	O60663 homo sapien
19	84.5	6.7	933	1 VGLB_HSV1	O04453 herpesvirus
20	84	6.6	310	1 TNFC_MARMO	O9jml0 marmota mon
21	83.5	6.6	885	1 VGLB_HSV2S	F24994 herpes simp
22	83	6.5	228	1 BIOD_PSAE	O9i614 pseudomonas
23	83	6.5	936	1 PHL1_YEAST	P39521 saccharomyc
24	82	6.5	258	1 RL2_ARATH	P46286 arabidopsis
25	82	6.5	369	1 LMXB_MESAU	O60554 mesocricetu
26	82	6.5	844	1 PHSG_DROME	O9xt19 drosophila
27	81.5	6.4	260	1 RL2_TOBAC	F25998 nicotiana t
28	81.5	6.4	260	1 TNF5_FELCA	O97605 felis silve
29	81	6.4	244	1 TNFC_HUMAN	O06643 homo sapien
30	81	6.4	273	1 OSAS_BOBUB	O09089 borrelia bu
31	80.5	6.3	280	1 TN13_HUMAN	O75888 homo sapien
32	80.5	6.3	281	1 TN10_HUMAN	P05591 homo sapien
33	80.5	6.3	675	1 PRTS_BOVIN	P07224 bos taurus

34	80.5	6.3	928	1 VGLB_HSVBP	P17471 bovine herp
35	80.5	6.3	932	1 VGLB_HSVBC	P12640 bovine herp
36	80.5	6.3	1565	1 DMN_HUMAN	O15061 homo sapien
37	80	6.3	547	1 RM56_HUMAN	P83111 homo sapien
38	80	6.3	664	1 UL47_HSV1F	P08313 herpes simp
39	80	6.3	693	1 UL47_HSV11	P10231 herpes simp
40	79.5	6.3	241	1 TN13_MOUSE	O9d777 mus musculus
41	79.5	6.3	814	1 CADF_HUMAN	P55291 homo sapien
42	79.5	6.3	4466	1 DYHC_ANTCR	P39057 anthocidari
43	79	6.2	261	1 TNF5_AOTTR	O9bdm3 actus trivi
44	79	6.2	261	1 TNF5_CALJA	O9bhm3 callithrix
45	79	6.2	280	1 TNF6_MACMU	O9myl6 macaca mula

## ALIGNMENTS

RESULT 1  
TN12\_HUMAN STANDARD; PRT; 249 AA.  
ID AC O43508; Q8MUZ7;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 12 (TNF-related weak inducer of apoptosis) (TWEAK) (APO3 ligand).  
GN TNFSF12 OR APO3L OR DR3LG.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_taxid=9606;  
OX [1]  
RN SEQUENCE FROM N.A., AND N-TERMINUS OF SOLUBLE FORM.  
RP TISSUE=Tonsil, and Fetal liver;  
RC MEDLINE=98070415; PubMed=9405449;  
RX Chicheportiche Y., Bourdon P.R., Xu H., Huu Y.-M., Scott H., Hession C., Garcia I., Browning J.L.;  
RA "TWEAK, a new secreted ligand in the tumor necrosis factor family that weakly induces apoptosis."  
RT J. Biol. Chem. 272:32401-32410(1997).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Fetal kidney;  
RC MEDLINE=98228355; PubMed=9560343;  
RA Marsters S.A., Sheridan J.P., Pitti R.M., Brush J., Goddard A., Ashkenazi A.;  
RX "Identification of a ligand for the death-domain-containing receptor APO3."  
RT Curr. Biol. 8:525-528(1998).  
RL [3]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Tonsil;  
RC Strausberg R.;  
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RL [4]  
RN FUNCTION.  
RP PubMed=10085077;  
RA Lynch C.N., Wang Y.C., Lund J.K., Chen Y.-W., Leal J.A., Wiley S.R.;  
RX "TWEAK-induces angiogenesis and proliferation of endothelial cells."  
RL J. Biol. Chem. 274:8455-8459(1999).  
CC -!- FUNCTION: Binds to FN14 and possibly also to TNFRSF12/APO3. Weak inducer of apoptosis in some cell types. Mediates NF-kappaB activation. May promote angiogenesis and the proliferation of endothelial cells.  
CC -!- SUBUNIT: HOMOTRIMER (POTENTIAL).  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted.  
CC -!- TISSUE SPECIFICITY: Highly expressed in adult heart, pancreas, skeletal muscle, brain, colon, small intestine, lung, ovary, prostate, spleen, lymph node, appendix and peripheral blood lymphocytes. Low expression in kidney, testis, liver, placenta, thymus and bone marrow. Also detected in fetal kidney, liver, lung and brain.  
CC -!- PTM: The soluble form derives from the membrane form

CC by proteolytic processing.  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to a  
 CC frameshift in position 125.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF030099; AAC51923.1; -  
 CC EMBL; AF055872; AAC39724.1; -  
 CC EMBL; BC019047; AAH19047.1; ALT\_FRAME.  
 CC Genew; HGNC:11927; TNFSF12.  
 CC MIN; 602695; -  
 CC DR InterPro; IPR000478; TNF\_family.  
 CC DR Pfam; PF00229; TNF; 1.  
 CC DR SMART; SM00207; TNF; 1.  
 CC R PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
 CC DR PROSITE; PS50049; TNF\_2; 1.  
 CC DR Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.  
 CC CHAIN 1 249  
 CC TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 CC MEMBER 12, MEMBRANE FORM.  
 CC CHAIN 94 249  
 CC TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 CC MEMBER 12, SECRETED FORM.  
 CC DOMAIN 1 21  
 CC CYTOPLASMIC (POTENTIAL).  
 CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 CC (POTENTIAL).  
 CC DOMAIN 43 249  
 CC EXTRACELLULAR (POTENTIAL).  
 CC SITE 93 94  
 CC CARBOHYD N-LINKED (GLCNAC...).  
 CC FT SEQUENCE 249 AA; 27216 MW; E560843361C28EBA CRC64;  
 CC  
 CC Query Match 100.0%; Score 1268; DB 1; Length 249;  
 CC Best Local Similarity 100.0%; Pred. No. 1.8e-99;  
 CC Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC Qy 1 MAARSQRGRGPGTALLVPLALGGLACGLALLVVLGSLASLQAQPEL 60  
 CC Db 1 MAARSQRGRGPGTALLVPLALGGLACGLALLVVLGSLASLQAQPEL 60  
 CC  
 CC Qy 61 VAEEDQDSELPQTEESQDPAFLNLRVPRSPKGRKTRARRAIAAHVEVHPRPGD 120  
 CC Db 61 VAEEDQDSELPQTEESQDPAFLNLRVPRSPKGRKTRARRAIAAHVEVHPRPGD 120  
 CC  
 CC Y 121 GAQAGVDGTVSGWEARINSSPLRYNQIGFIVTRAGLYLYCQVHFDEGKAVYLKLD 180  
 CC Db 121 GAQAGVDGTVSGWEARINSSPLRYNQIGFIVTRAGLYLYCQVHFDEGKAVYLKLD 180  
 CC  
 CC Qy 181 LLDVGVLRCLREEFSATASSLGQLRLCQVSGLLALRPGSSLRIRTLPAHLKAAPFL 240  
 CC Db 181 LLDVGVLRCLREEFSATASSLGQLRLCQVSGLLALRPGSSLRIRTLPAHLKAAPFL 240  
 CC  
 CC Qy 241 TYFGLFQVH 249  
 CC Db 241 TYFGLFQVH 249  
 CC  
 CC RESULT 2  
 CC ID TN12 MOUSE STANDARD; PRT; 225 AA.  
 CC AC 054907; Q9CTP2;  
 CC DT 15-JUN-2002 (rel. 41, Created)  
 CC DT 15-JUN-2002 (rel. 41, Last sequence update)  
 CC DT 15-JUN-2002 (rel. 41, Last annotation update)  
 CC DE Tumor necrosis factor ligand superfamily member 12 (TNF-related weak  
 CC inducer of apoptosis) (TWEAK) (Fragment).  
 CC GN TNFSF12.  
 CC OS Mus musculus (Mouse).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peritoneal macrophage;  
 RX MEDLINE=98070415; PubMed=9405449;  
 RA Chicheportiche Y., Bourdon P.R., Xu H., Hsu Y.-M., Scott H.,  
 RT Hession C., Garcia I., Browning J.L.;  
 RT "TWEAK, a new secreted ligand in the tumor necrosis factor family that  
 RT weakly induces apoptosis";  
 RL J. Biol. Chem. 272:32401-32410(1997).  
 RN [2]  
 RP SEQUENCE OF 83-225 FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Retina;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavanta H.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontseki S.,  
 RA Hayaehizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 CC -!- FUNCTION: Induces of apoptosis in some cell types. Promotes angiogenesis and  
 CC the proliferation of endothelial cells. Mediates NF-KappaB  
 CC activation (By similarity).  
 CC -!- SUBUNIT: Homotrimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.  
 CC -!- PTM: The soluble form is produced from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AF030100; AAC53517.1; -  
 CC EMBL; AK020909; BAB32249.1; -  
 CC MGD; MGI:1196259; Tnfsf12.  
 CC InterPro; IPR000478; TNF\_family.  
 CC Pfam; PF00229; TNF; 1.  
 CC DR SMART; SM00207; TNF; 1.  
 CC DR PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
 CC DR PROSITE; PS50049; TNF\_2; 1.  
 CC DR Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.  
 CC NON TER 1 1  
 CC CHAIN <1 225 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 CC MEMBER 12, MEMBRANE FORM.  
 CC CHAIN 70 225 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 CC MEMBER 12, SECRETED FORM (BY SIMILARITY).  
 CC TRANSMEM <1 21 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 CC (POTENTIAL).  
 CC DOMAIN 22 225 EXTRACELLULAR (POTENTIAL).  
 CC SITE 69 70 CLEAVAGE (BY SIMILARITY).  
 CC FT

DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; P850049; TNF_2; 1.
KW	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT	CHAIN 1 272
FT	CHAIN 111 272
FT	DOMAIN 1 23
FT	TRANSMEM 24 44
FT	DOMAIN 45 272
FT	SITE 110 111
FT	DISULFID 190 229
FT	CARBOHYD 124 124
FT	CARBOHYD 146 146
FT	CARBOHYD 251 251
SQ	SEQUENCE 272 AA; 30862 MW; 5409F24A8E53CCD7 CRC64;

Query Match 8.6%; Score 109.5; DB 1; Length 272;  
 Best Local Similarity 26.4%; Pred. No. 0.037;  
 Matches 42; Conservative 26; Mismatches 58; Indels 33; Gaps

QY	104 RRAIAAHYEHPGODGAQGVDGTVSGW-EEARINSSSPLYRNPQIGEFIVTRAGLXY 162
DB	133 RQPIATHLA-----GVKSTNTTVRLVKMTTSYAPTSLSIYHE--GKLKVKAAGLY 182
QY	163 LYCQVFHDEGKA-----VYLKDLLVDGVLALCLFEFSATASSLGPQLRCQV-- 212
DB	183 IYSQVSFCTKAASAPFTYIYLPMEEDRL-LMGLDTHSTSTA-----LCLEQS 233
QY	213 ---SGLLARPGSSLRIRTLPLWAHLKAAPFLTYFGLFQV 248
DB	234 IREGGVFELRQGDVMFVNVTDSAVNVNPGNTYFGMKL 272

RESULT 4  
 TNF5\_CANFA STANDARD; PRT; 260 AA.  
 ID TNF5\_CANFA STANDARD; PRT; 260 AA.  
 AC O976%  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand).  
 GN TNF5F5 OR CD40LG OR CD40L.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 ON NCBI\_TaxID=9615;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Hosie M.H., Willett B.J.;  
 RT "Adjuvant properties of canine CD40L.";  
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.  
 CC -! FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).  
 CC -! SUBUNIT: HOMOTRIMER (By similarity).  
 CC -! SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).  
 CC -! PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).  
 CC -! SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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DR	EMBL; AF086711; AAD04375.1; --
----	--------------------------------







PFam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF abc; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF; 1; FALSE\_NEG.  
 DR PROSITE; PS00049; TNF; 2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;  
 KW Alternative splicing.  
 CHAIN 1 240

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 MEMBER 14, MEMBRANE FORM.  
 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 MEMBER 14, SOLUBLE FORM.  
 CYTOPLASMIC (POTENTIAL).  
 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)  
 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 CLEAVAGE (POTENTIAL).  
 POTENTIAL (GLCNAC... ).  
 MISSING (IN ISOFORM 2).  
 L -> V (IN REF. 4).  
 E -> K (IN REF. 2).  
 CONFLICT 214 214  
 SEQUENCE 240 AA; 26351 MW; 4900BF67E1390B39 CRC64;

Query Match 7.2%; Score 91.5; DB 1; Length 240;  
 Best Local Similarity 25.0%; Pred. No. 1;  
 Matches 44; Conservative 18; Mismatches 47; Indels 67; Gaps 7;

QY 5 RSRRRG-RRCEPTGALLVPLALGLGALACLGALLAVVSLGSRASLSAQPAQOEELVAE 63  
 DB 26 KSHRRQSCSVARVGLGLL-LMGAGLAVQVWFLQLHRLG-----EMV-- 69  
 QY 64 EDQDPSELNPQTESQDPAPFLNLRPRRSGPKRTRARRAIAAHVEVHPRGQGAQ 123  
 DB 70 -----TRLPDGPAGSWEQLIQERS-----HEVNPAAHLTCAN 102  
 QY 124 AGVDGTVSGWEARINSSSPRYNRQI-----GFIVTRAGLYLYYCOV 167  
 DB 103 SSLTG-----SGPLLWETQLGLAFLRGLSYHDGALVTVTKAGYYIYSKV 147

RESULT 8  
 CG22 ANTMA STANDARD; PRT; 441 AA.  
 AC P34801;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE G2/mitotic-specific cyclin 2.  
 S Antirrhinum majus (Garden snapdragon).  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.  
 OX NCBI\_TaxID=4151;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94148008; PubMed=8313906;  
 RA Robert P.R., Coen E.S., Murphy G.P., Doonan J.H.;  
 RT "Patterns of cell division revealed by transcriptional regulation of  
 genes during the cell cycle in plants."  
 RL EMOB J. 13:616-624(1994).  
 CC -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M  
 (MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADILY DURING G2  
 AND ARE ABRUPTLY DESTROYED AT MITOSIS.  
 CC -!- SUBUNIT: INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KINASES TO FORM  
 A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT  
 IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.  
 CC -!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS  
 ABRUPTLY DESTROYED AT MITOSIS.  
 CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.  
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 or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL: X76123; CAA53729.1; -  
 DR FIR; S41710; S41710.  
 DR HSSP; P30274; IVIN.  
 DR InterPro; IPR004366; Cyclin.  
 DR InterPro; IPR004367; Cyclin\_Cterm.  
 DR Pfam; PF00134; cyclin; 1.  
 DR Pfam; PF02984; cyclin\_C; 1.  
 DR SMART; SM00385; CYCLIN; 2.  
 DR PROSITE; PS00292; CYCLINS; 1.  
 DR Cyclin; Cell cycle; Cell division; Mitosis.  
 KW Cyclin; Cell cycle; 49205 MW; E6E4C037C98880A7 CRC64;  
 SQ SEQUENCE 441 AA; 49205 MW; E6E4C037C98880A7 CRC64;

Query Match 7.1%; Score 90; DB 1; Length 441;  
 Best Local Similarity 23.8%; Pred. No. 2.8;  
 Matches 67; Conservative 42; Mismatches 102; Indels 70; Gaps 14;

QY 1 MAARRSQRR-----RGRGEPGTALLVPLALGLGALACLGLL----- 38  
 DB 26 MAYEKNRRALGDIGNVTVRGVEKALPOVSRPITRGF-----CAQLIANAEAAAAENN 80  
 QY 39 ---LAVVSLGSRASLS-----AQEPAQEELVAEEDQPSLNQTESQDPAPFLNLRV 90  
 DB 81 KNSLAVNAKGADGALPIKRAVARVPQKTKVSKPOEIIIEISPDTEKKK--APVLEKEIT 138  
 QY 91 PRRS-----APKGRKTRARRAIAAHVEVHPRPGO-----DGAQAGVDGTVSGWEE----- 135  
 DB 139 GEKSLKKKALTSTLTARSKAASV-VRTAPKEQIVDIDADVNDLAVVEYEDVMYKFY 197  
 QY 136 -ARINSSSPRY---NRQGEFIVTRAGLYLYYCOVFD---EGKAVYKLKDLVLDGVL 188  
 DB 198 KSAENDSRPHDYMSQPEINEKM--RAILLDLVQVHYKFEELSPETLYLTIN-IVDRYLA 254  
 QY 189 LRC-----LEEFSAATASLGPQLRCLQVSGLLALRPGS 222  
 DB 255 SKTTSRRELQGLGSSMLIASKEYEINWAEVNDLVCIISDGS 295

RESULT 9  
 JIPI\_MOUSE STANDARD; PRT; 707 AA.  
 ID JIPI\_MOUSE  
 AC Q9WV19; Q9WV18; Q9WV17; Q9RIH9; Q9RI21; Q35145;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE C-jun-amino-terminal kinase interacting protein 1 (JNK-interacting  
 protein 1) (JIP-1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1)  
 DE (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1).  
 GN MAPK8IP1 OR PRKMBIP OR Jip1 OR IB1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.  
 RC TISSUE=Brain;  
 RX MEDLINE=97382333; PubMed=9235893;  
 RA Dickens M., Rogers J.S., Cavanagh J., Raitano A., Xia Z.,  
 RA Halpern J.R., Greenberg M.E., Sawyers C.L., Davis R.J.;  
 RT "A cytoplasmic inhibitor of the JNK signal transduction pathway."  
 RL Science 277:693-696(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS JIP-1B; JIP-1C; JIP-1D AND JIP-1E).  
 RC STRAIN=BALB/c; TISSUE=Brain;  
 RX MEDLINE=99196470; PubMed=10098834;  
 RA Kim I.-J., Lee K.-W., Park B.Y., Lee J.-K., Park J., Choi I.Y.,  
 RA Eom S.-J., Chang T.-S., Kim M.J., Yeom Y.I., Chang S.K., Lee Y.-D.,  
 RA Choi E.-J., Han P.-L.;  
 RT "Molecular cloning of multiple splicing variants of JIP-1

```
Query Match      6.9%; Score 87; DB 1; Length 291;
Best Local Similarity 27.2%; Pred. No. 3.1;
Matches 31; Conservative 16; Mismatches 53; Indels 14; Gaps

QY 58 EELVAEEDQPSELNPQTESQDPAFLNRLVPRPSAP--KGRKTRARRATAAHVEVHP 115
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 93 EEVTLRFTDTISTVPEKQLSTPLP---RGGRPQVAAHITGTRRSNSALIP-----143

QY 116 RPGGDGAQAGVDGTSGWEARINSSSPRYNRQIGFEIVTRAGLYYLVCQVHF 169

DB 144 -ISKDGKTLTG--OKIESWSSRRKGHSFLLNHVLPRNGELVIYEOGLYIYSOTVF 194
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RESULT 13
Y497_MYCTU
ID Y497_MYCTU STANDARD; PRT; 310 AA.
AC Q11162;
DC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein RV0497.
GN RV0497 OR MT0517 OR MTCY20G9.23.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacterium
OX NCBI_TaxID=1773;
[1]
RN RP SEQUENCE FROM N.A.
RP STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
[2]
RN RP SEQUENCE FROM N.A.
RP STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: TO M.LEPRAE ML2433.
CC
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CC EMBL; Z77162; CAB00923.1; -;  
 DR EMBL; AE006952; AAK44740.1; -;  
 DR TIGR; MT0517; -;  
 DR Tuberculin; R0497; -;  
 KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 231 251 POTENTIAL.  
 FT TRANSMEM 257 277 POTENTIAL.  
 FT TRANSMEM 286 306 POTENTIAL.  
 FT DOMAIN 33 39 POLY-ARG.  
 FT DOMAIN 197 202 POLY-ALA.  
 SQ SEQUENCE 310 AA; 33092 MW; 49540278694DF5C2 CRC64;

Query Match 6.9%; Score 87; DB 1; Length 310;  
 Best Local Similarity 24.0%; Pred. No. 3.3;  
 Matches 72; Conservative 24; Mismatches 90; Indels 114; Gaps 16;

3 ARRSRRG-----RRGPGTALLVPLALGLGLALACLGLLLA 40  
 |||:||||  
 32 ARRRRRRGSDAITVAELTGEIPIIRDDHHAGPDAAHSQSPAANG----- 79  
 41 VVSLGSRASLSAQPAQELVAEE-----DODPSLNQTEESODPAPFLNLRVPR 92  
 80 -VQGEAAPQAPPAVPAEQ-VAEPRTVYNSQPEPRWPKSPQDRRESGPELSEYRPL 137  
 93 R-----SAPGKRKTRARRAI---AAHY-----EVHPRQDQ----- 121  
 138 RHTSDRAPAGPPSGAEHMSDPVEHYPDLDVLDTEVGEAAETEVRAQPCGRGHA 197  
 122 --AQQVDGTVSGWEEARINSS-----PLRYNRQIGEIFIVTR-----AGLYLYLCQV 167  
 198 AAAAAGTDEGDGAARVARRALDVPVTLWR---GALVLIQSILAVAFAGLGF-----I 249  
 168 HFDE---GKAVYLKLDL---LVDGVLAIRCLEEFSAF-----AASLIGPQLRLCQ 211  
 250 AFDQLWRNNSIVALVLSVMVLGLVSVRAVRKTEDIASTLIAVAVGALITLGP-LALLQ 308

RESULT 14  
 ID TNFC\_MACEU STANDARD; PRT; 250 AA.  
 AC Q9XT47;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor  
 DE necrosis factor ligand superfamily member 3).  
 GN LTB OR TNFSP3 OR TNFC.  
 OS Macropus eugenii (Tamar wallaby).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
 OX NCBI\_TaxID=9315;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Harrison G.A., Cooper D.W., Deane E.M.;  
 RL "cDNA sequence of the tamar wallaby lymphotoxin beta chain.";  
 RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Cytokine that binds to LTRP/TNFSF3. May play a specific  
 CC role in immune response regulation. Provides the membrane anchor  
 CC for the attachment of the heterotrimeric complex to the cell  
 CC surface.  
 CC -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or  
 CC (less prevalent) two LTA and one LTB subunits (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC EMBL; AF119337; AAD41774.1; -;  
 DR HSSP; P01374; ITNR.  
 DR InterPro; IPR003636; TNF abc.  
 DR InterPro; IPR00478; TNF\_family.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_abc; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
 FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 27 47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 48 250 EXTRACELLULAR (POTENTIAL).  
 FT CARBOHYD 228 228 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 250 AA; 26143 MW; AD37FB975452FE84 CRC64;

Query Match 6.8%; Score 86.5; DB 1; Length 250;  
 Best Local Similarity 21.2%; Pred. No. 2.8;  
 Matches 65; Conservative 31; Mismatches 95; Indels 115; Gaps 12;

QY 1 MAARRSQRGRGEGECTALLVPLALGLALACLGLLAVSLGSRASLSAQEPQAEEL 60  
 DB 1 MGAPGUETRAG--GPNKSYLLASVG-----AAVLGTLISVITVTLVLAIMPQGGQ 54  
 QY 61 VAEEDODPS-----ELNPQTEESQDPAPFLNLRVPRSPAPKGRKTRARRAI 107  
 DB 55 VA---DPSGPGQLLQQLGFHKLPEVESRDLSPIPAAHLIGIAKSSHGLR----- 102  
 QY 108 AAHYEVHPRQDGAQAGVDGTVSGWEEARINSSPLRYNRQIGEIFIVTRAGLYLYCQV 167  
 DB 103 -----WVSGYEAFKSGT--QFLGDEGLLALPDQGIYFLYCHI 139  
 QY 168 HF-----DEGKAVYLKLDLVDGVLAIRCLEEFSAFATAASSLG-PQLRL- 209  
 DB 140 GYGRAPSGGEGEQRSGQAGDPGVPTLSSQL-----FRAGASGSGEPELLQ 186  
 QY 210 -----CQVSGLLALRPSSLRITLPWAHLKAAPF---LTY 242  
 DB 187 GFETVTPVQHARGVGQGLWYATVFGGLVQLRGGEKIYVNV---SHLELVDFRRGKTF 243

RESULT 15  
 ID YQFB\_BACSU STANDARD; PRT; 139 AA.  
 AC P54467;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein yqfb.  
 GN YQFB.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168 / JH642;  
 RX MEDLINE=97124195; PubMed=8969508;  
 RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,  
 RA Kobayashi Y.;

RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of  
 the Bacillus subtilis genome containing the skin element and many

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OM protein - protein search, using sw model

Run on: April 12, 2003, 08:38:15 ; Search time 32 Seconds  
(without alignments)  
1603.304 Million cell updates/sec

Title: US-09-905-810-2

Perfect score: 1268  
Sequence: 1 MAARRSRRRRGRRGPTAL.....PWAHLKAAPLTYFGLPQVH 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 671580 seqs, 206047115 residues

al number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	116	9.1	325	5	Q9V5G2	Q9v5g2 drosophila
2	97	7.6	643	16	Q9K217	Q9k217 streptomyc
3	95	7.5	375	16	Q9RRH5	Q9rrh5 deinococcus
4	94	7.4	937	16	Q93JDI	Q93jdi streptomyc
5	93.5	7.4	776	16	Q9RJ01	Q9rj01 streptomyc
6	93	7.3	378	16	Q9AAB9	Q9aab9 caulobacter
7	92.5	7.3	707	11	Q925J8	Q925j8 mus musculu
8	92	7.3	977	4	Q8TE11	Q8tel1 homo sapien
9	91.5	7.2	212	16	Q86312	Q86312 mycobacteri
10	90.5	7.1	1100	2	Q937L3	Q937l3 deinococcus
11	89	7.0	522	10	Q9FTN7	Q9ftn7 oryza sativ
12	89	7.0	664	16	Q9HTN7	Q9hvt9 pseudomonas
13	89	7.0	854	16	Q9E2P0	Q9f2p0 streptomyc
14	88	6.9	655	16	Q9FBR7	Q9fbr7 streptomyc
15	87.5	6.9	274	10	Q949L6	Q949l6 beta vulgar
16	87.5	6.9	5192	2	Q93TW9	Q93tw9 stigmatella

17	87	6.9	267	2	Q24793	Q24793 borrelia ga
18	87	6.9	273	2	Q44962	Q44962 borrelia bu
19	87	6.9	273	2	Q31376	Q31376 borrelia ga
20	87	6.9	427	10	Q8S9W3	Q8s9w3 oryza sativ
21	87	6.9	445	12	Q98174	Q98174 molluscum c
22	87	6.9	565	16	Q9KV66	Q9kv66 streptomyc
23	86.5	6.8	225	13	Q9IB42	Q9ib42 paralicthys
24	86.5	6.8	308	4	Q96M87	Q96m87 homo sapien
25	86.5	6.8	331	10	Q942P9	Q942p9 oryza sativ
26	86.5	6.8	536	4	Q9HB96	Q9hb96 homo sapien
27	86.5	6.8	755	16	Q9RTB1	Q9rtb1 deinococcus
28	86.5	6.8	810	16	Q97N72	Q97n72 streptococc
29	86	6.8	287	13	Q90WT9	Q90wt9 gallus gall
30	86	6.8	614	4	Q8WU14	Q8wu14 homo sapien
31	86	6.8	855	4	Q9NYK9	Q9nyk9 homo sapien
32	86	6.8	878	4	Q9UFU7	Q9ufu7 homo sapien
33	86	6.8	1294	5	Q9GY29	Q9gy29 leishmania
34	86	6.8	1837	5	Q967R4	Q967r4 caenorhabdi
35	85.5	6.7	361	4	Q9BQ88	Q9bq88 homo sapien
36	85.5	6.7	412	4	Q8WY10	Q8wy10 homo sapien
37	85	6.7	272	2	Q31374	Q31374 borrelia ga
38	85	6.7	431	10	Q23088	Q23088 arabidopsis
39	84.5	6.7	402	2	Q51973	Q51973 pseudomonas
40	84.5	6.7	450	16	Q8Y1A3	Q8y1a3 ralstonia s
41	84.5	6.7	748	5	Q8T2Y0	Q8t2y0 trypanosoma
42	84.5	6.7	9376	2	Q8S168	Q8s168 pseudomonas
43	84	6.6	260	10	Q9SD27	Q9sd27 arabidopsis
44	84	6.6	274	2	Q45194	Q45194 borrelia ga
45	84	6.6	532	4	Q96AP3	Q96ap3 homo sapien

#### ALIGNMENTS

#### RESULT 1

Q9V5G2 ID Q9V5G2 PRELIMINARY; PRT; 325 AA.

AC Q9V5G2; DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE CG12919 protein.

GN CG12919.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos L.G.,  
RA Abrial J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Molyshina N.V., Mobaraj C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moysa M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., M.G.,  
 RA Palazolo M., Pittman G.S., Fan S., Pollard J., Furi V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasarman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AF58848.1; --  
 DR FlyBase; FBgn033483; CG12919.  
 DR InterPro; IPR000478; TNF\_family.  
 DR SMART; SM00207; TNF; 1.  
 PROSITE; PS00251; TNF.1; 1.  
 PROSITE; PS50049; TNF.2; 1.  
 SQ SEQUENCE 325 AA; 35862 MW; 685CCB69694FlA3A CRC64;

Query Match 9.1%; Score 116; DB 5; Length 325;  
 Best Local Similarity 25.4%; Pred. No. 0.029;  
 Matches 57; Conservative 32; Mismatches 97; Indels 38; Gaps 10;

Qy 47 RASLSAQEPAQELVAE-----EDQPSSELNQTESQDPAPFLNR-----LVPR 92  
 Db 118 KRSRSIADVRNEEQIGNHTLEQKSENEATSKES--PAPLHRRRMRHRLLVKRG 175  
 Qy 93 RSAPKGRKTRARRATAAHVEHPRPGQGAQAGVDGTSGWEARINSSPLRYNRQICE 152  
 Db 176 ESLLSARSEDSP--AAHFLSSRRRHQSGM-GYHGDYVIGNDNERNYSYQG-HFQTRDGV 231  
 Qy 153 FIVTRAGLYLYYLCVQV-----HFDEKAVYKLDLLVDGVLALRCLEFSATASSLGPQL 207  
 Db 232 LTVNTGLYVYAQICYNNSHQNGFVFE-----QGDTPFLQCLN-----TVPTNMPHKV 281  
 Qy 208 RLCQVSGLLALRPSSLRIRTL---PWAHLKAAPLTYFGLFOV 248  
 Db 282 HTCHTSGLIHLERNRIHLKDINDRNAVLREGNRSYFGIFKV 325

RESULT 2  
 Q9KZ17 PRELIMINARY; PRT; 643 AA.  
 Q9KZ17;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical protein SC02220.  
 GN SC02220 OR SC1087.15.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RC Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kieser I., Lark L., Murphy L., Oliver K., O'Neil S.,  
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3(2).";

RL Nature 417:141-147(2002).  
 DR EMBL; AL355752; CAB90868.1; --  
 KW Hypothetical protein.  
 SQ SEQUENCE 643 AA; 66537 MW; 1217A5C8E3CD419 CRC64;  
 Query Match 7.6%; Score 97; DB 16; Length 643;  
 Best Local Similarity 24.4%; Pred. No. 3.3;  
 Matches 54; Conservative 21; Mismatches 102; Indels 44; Gaps 6;  
 Qy 25 ALGLGALACLLGLLAVVSLGSRASLSAQEPAQELVAEEDQPSSELNQTESQDPAPF 84  
 Db 227 ALVAGALVVCAGLLGLPGDGGAPPAQYQNPAAEAALDPGRLTKAAPAAWETSAR 286  
 Qy 85 LNLRLVRRSPAPGRKTRARRATAAHVEHPRPGQGAQAGVDGTSGWEARINSSPL 144  
 Db 287 TDFSVPARGGLTGDELLRALA-----VWARPGESVGVSATPGTATG-----GP- 332  
 Qy 145 RYNRQICEFIVTRAGLYLYYLCVQVHFDEKAVYKLDLLVDGVLALRCLEFSATASSL- 203  
 Db 333 -----AGPPOLLYAGEVDTARVV-----VLHGLRLVRVAEPKDSAGAALD 374  
 Qy 204 -----GPQLRLCQVSGLLALRPSSLRIRTLTPWAHLKAA 237  
 Db 375 FARTDGAAGRAATAVVLG-----RADGNVRYLTAPWVTKAAA 411

RESULT 3  
 Q9RRH5 PRELIMINARY; PRT; 375 AA.  
 ID Q9RRH5  
 AC Q9RRH5  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein DR2516.  
 GN DR2516.  
 OS Deinococcus radiodurans.  
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;  
 OC Deinococcaceae; Deinococcus.  
 OX NCBI\_TaxID=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R1;  
 RC MEDLINE=20036896; PubMed=10567266;  
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,  
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.";  
 RL Science 286:1571-1577(1999).  
 DR EMBL; AE002081; AAF12062.1; --  
 DR TIGR; DR2516; --  
 KW Hypothetical protein; Complete proteome.

Qy 4 RRSORRRGRGEGPT--ALLVPLALGLALACLLGLLAVVSLGSRASLSAQE-PAQEEL 60  
 Db 24 RRPGRAPGRGQPGSHPAARQLRADLCAALA-----LVADVVTTRPTLPAGELPTLLDL 77  
 Qy 61 VAEDQPSSELNQTESQDPAPFLNLRPRRSPAPKGRKTRARRATAAHVEHPR-PGQ 119  
 Db 78 AR-----QDLESDDSP-----TDLAVQARATFRLPGD 108  
 Qy 120 DGAQAG--VDGTSGWEARINSSPLRYNRQICE-----PIVTRAGLYLY----- 164  
 Db 109 PGAGFGHPISGTLAGLE--RLSAASLRAHWARFQGRGVLGVADADAQEVYELVAGLFA 166

Query Match 7.5%; Score 95; DB 16; Length 375;  
 Best Local Similarity 23.9%; Pred. No. 2.5;  
 Matches 64; Conservative 26; Mismatches 76; Indels 102; Gaps 12;



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; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: TWEAK fusion protein construct
US-09-883-777-2

Query Match      84.1%; Score 1066; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.8e-89;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0

      43 SLGRASLSAQEPAQEELVAEEDQPSSELNPQTEESQDPAPFLNLVPRRSAPKGRKTR 102
      |||
      67 SLGRASLSAQEPAQEELVAEEDQPSSELNPQTEESQDPAPFLNLVPRRSAPKGRKTR 126

QY      103 ARRATAAHYEVHPRPGDGAQGVDTGTVSGWEEARINSSPLRYNRQIGEFIVTRAGLYY 162
DB      127 ARRATAAHYEVHPRPGDGAQGVDTGTVSGWEEARINSSPLRYNRQIGEFIVTRAGLYY 186

QY      163 LYCVHFDEGKAVYKLKDLLVDGVLAALCLREFSATAASSLGQPLRLCQVSGLLALRPGS 222
DB      187 LYCVHFDEGKAVYKLKDLLVDGVLAALCLREFSATAASSLGQPLRLCQVSGLLALRPGS 246

QY      223 SLRITLPWAHLKAAPFLTYFGLFQVH 249
DB      247 SLRITLPWAHLKAAPFLTYFGLFQVH 273

RESULT 5
US-09-905-810-1
; Sequence 1, Application US/09905810
; Patent No. US20020015703A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: RENNERT, Paul
; TITLE OF INVENTION: Antagonists of Tweak and of Tweak
; TITLE OF INVENTION: Receptor and Their Use to Treat Immunological Disorders
; FILE REFERENCE: A068 US
; CURRENT APPLICATION NUMBER: US/09/905,810
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/01044
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/116,168
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Murine
US-09-905-810-1

Query Match      80.4%; Score 1020; DB 10; Length 225;
Best Local Similarity 88.8%; Pred. No. 2.2e-85;
Matches 199; Conservative 9; Mismatches 16; Indels 0; Gaps 0

QY      26 LGGLALACLLLVAVSLGRASLSAQEPAQEELVAEEDQPSSELNPQTEESQDPAPFL 85
DB      2 LSLGLALACLLLVVWSLGSWATLSAQEPSQEELTAEDRREPPLNPQTEESQDWPFL 61

QY      86 NRLVPRRSAPKGRKTRARRATAAHYEVHPRPGDGAQGVDTGTVSGWEEARINSSPLR 145
DB      62 EQLVPRRSAPKGRKTRARRATAAHYEVHPRPGDGAQGVDTGTVSGWEEATKINSSPLR 121

QY      146 YNRQIGEFIVTRAGLYYLYCQVHDEGKAVYKLKDLLVDGVLAALCLREFSATAASSLG 205

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```

RESULT 9
US-09-027-287-39
; Sequence 39, Application US/09027287A
; Patent NO. US20020064869A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; TITLE OF INVENTION: Apoptosis Inducing Molecule II
; FILE REFERENCE: 1488.0650004
; CURRENT APPLICATION NUMBER: US/09/027,287A

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Query Match 7.3%; Score 92.5; DB 10; Length 208;  
Best Local Similarity 25.0%; Pred. No. 0.62;  
Matches 41; Conservative 18; Mismatches 38; Indels 67; Gaps 7;

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QY 22 VPLA-LGLGLALACGLLLAV-----VSLGSRASLSAQEPAQEELVAEEDQDPSELNPOT 75
Db 1 IPRAVGLGLLLMLGAGLAVQGVFLLQLHWRLG-----EMV-----T 38
QY 76 EESQDPAPFLNLRPRRSPAPKGRKTRARRATAAHHVEVHPRPQDGAQAGVDGTVSGWEE 135
Db 39 RLDPDGAGSWEQIQERRS-----HEVNPAAHLTGANSSLTG----- 75
QY 136 ARINSSPLRYNRQI-----GEFIVTRAGLYLYLCOV 167
Db 76 ----SGPLLWETQLGLAFRLGSLYHDGALVVTKAGYIIYSKV 115

RESULT 11
US-09-967-604-6
; Sequence 6, Application US/09967604
; Publication No. US20030060605A1
; GENERAL INFORMATION:
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; APPLICANT: WARE, CARL F.
; TITLE OF INVENTION: LIGAND FOR HERPES SIMPLEX VIRUS ENTRY MEDIATOR AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 051501/0278793
; CURRENT APPLICATION NUMBER: US/09/967,604
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/549,096
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 08/898,234
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/051,964
; PRIOR FILING DATE: 1997-07-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-967-604-6

Query Match
Best Local Similarity 7.2%; Score 91.5; DB 9; Length 240;
Matches 44; Conservative 18; Mismatches 47; Indels 67; Gaps 7;

QY 5 RSQRRG-RRGPGTALLVPLALGGLALACGLLLAVVSLGSRASLSAQEPAQEELVAE 63
Db 26 RSHRRQSCSVARVGLGLLL-LLMGAGLAVQGVFLLQLHWRLG-----EMV-- 69
64 EDQDPSELNPQTEESQDPAPFLNLRPRRSPAPKGRKTRARRATAAHHVEVHPRPQDGAQ 123
70 -----TRLPDGAGSWEQIQERRS-----HEVNPAAHLTGAN 102
124 AGVDGTVSGWEEARINSSPLRYNRQI-----GEFIVTRAGLYLYLCOV 167
103 SSLTG-----SGPLLWETQLGLAFRLGSLYHDGALVVTKAGYIIYSKV 147

RESULT 12
US-10-151-882-45
; Sequence 45, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 240
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-151-882-45

Query Match
Best Local Similarity 7.2%; Score 91.5; DB 9; Length 240;
Matches 44; Conservative 18; Mismatches 47; Indels 67; Gaps 7;

QY 5 RSQRRG-RRGPGTALLVPLALGGLALACGLLLAVVSLGSRASLSAQEPAQEELVAE 63
Db 26 RSHRRQSCSVARVGLGLLL-LLMGAGLAVQGVFLLQLHWRLG-----EMV-- 69
64 EDQDPSELNPQTEESQDPAPFLNLRPRRSPAPKGRKTRARRATAAHHVEVHPRPQDGAQ 123
70 -----TRLPDGAGSWEQIQERRS-----HEVNPAAHLTGAN 102
124 AGVDGTVSGWEEARINSSPLRYNRQI-----GEFIVTRAGLYLYLCOV 167
103 SSLTG-----SGPLLWETQLGLAFRLGSLYHDGALVVTKAGYIIYSKV 147

RESULT 13
US-09-027-287-2
; Sequence 2, Application US/09027287A
; Patent No. US20020064869A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; TITLE OF INVENTION: Apoptosis Inducing Molecule II
; FILE REFERENCE: 1488.0650004
; CURRENT APPLICATION NUMBER: US/09/027,287A
; CURRENT FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: US 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: US 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: US 60/030,157
; EARLIER FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: US 60/013,923
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-027-287-2

Query Match
Best Local Similarity 7.2%; Score 91.5; DB 10; Length 240;
Matches 44; Conservative 18; Mismatches 47; Indels 67; Gaps 7;

QY 5 RSQRRG-RRGPGTALLVPLALGGLALACGLLLAVVSLGSRASLSAQEPAQEELVAE 63
Db 26 RSHRRQSCSVARVGLGLLL-LLMGAGLAVQGVFLLQLHWRLG-----EMV-- 69
64 EDQDPSELNPQTEESQDPAPFLNLRPRRSPAPKGRKTRARRATAAHHVEVHPRPQDGAQ 123
70 -----TRLPDGAGSWEQIQERRS-----HEVNPAAHLTGAN 102
124 AGVDGTVSGWEEARINSSPLRYNRQI-----GEFIVTRAGLYLYLCOV 167
103 SSLTG-----SGPLLWETQLGLAFRLGSLYHDGALVVTKAGYIIYSKV 147

RESULT 14
US-09-252-656B-2
; Sequence 2, Application US/09252656B
; Patent No. US20020081647A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
```

APPLICANT: Ruben, Steven M.  
APPLICANT: Zhang, Jun  
APPLICANT: Ullrich, Stephen  
APPLICANT: Zhai, Yifan  
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
FILE REFERENCE: 1488.0650006  
CURRENT APPLICATION NUMBER: US/09/252,656B  
CURRENT FILING DATE: 1999-02-19  
PRIOR APPLICATION NUMBER: US 60/075,409  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 09/027,287  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 09/003,886  
PRIOR FILING DATE: 1998-01-07  
PRIOR APPLICATION NUMBER: US 08/822,953  
PRIOR FILING DATE: 1997-03-21  
PRIOR APPLICATION NUMBER: US 60/013,923  
PRIOR FILING DATE: 1996-03-22  
PRIOR APPLICATION NUMBER: US 60/030,157  
PRIOR FILING DATE: 1996-10-31  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 240  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-252-656B-2

Query Match 7.2%; Score 91.5; DB 10; Length 240;  
Best Local Similarity 25.0%; Pred. No. 0.93; Mismatches 47; Indels 67; Gaps 7;  
Matches 44; Conservative 18;  
QY 5 RSQRRRG-RRGEPGTALLVPLALGLGLALACLGLLAVVSLGSRASLSAQEPAQEELVAE 63  
DB 26 RSHRRQSCSVARVGLGLLL-LMGAGLAVQGFLLQLHWRLG-----EMV-- 69  
QY 64 EDQDPSLNQTEESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGDGAQ 123  
DB 70 -----TRLPDGPAGSWEQLIQERRS-----HEVNPAAHLTGAN 102  
QY 124 AGVDGTVSGWEERINSSPLRYNRQI-----GEFIVTRAGLYLYCOV 167  
DB 103 SSLTG-----SGPFLWETQLGLAFRLGLSYHDGALVVTKAGYIIYSKV 147

RESULT 15  
US-10-066-209-4  
Sequence 4, Application US/10066209  
Patent No. US2002011510A1  
GENERAL INFORMATION:  
APPLICANT: Brigham-Burke, Michael R.  
APPLICANT: Young, Peter R.  
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND  
TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2  
FILE REFERENCE: GH-50030-D1  
CURRENT APPLICATION NUMBER: US/10/066,209  
CURRENT FILING DATE: 2001-10-25  
PRIOR APPLICATION NUMBER: 09/072,993  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/055,513  
PRIOR FILING DATE: 1997-08-13  
PRIOR APPLICATION NUMBER: 60/056,980  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/057,550  
PRIOR FILING DATE: 1997-08-29  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 240  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
US-10-066-209-4

Query Match 7.2%; Score 91.5; DB 12; Length 240;  
Best Local Similarity 25.0%; Pred. No. 0.93; Mismatches 47; Indels 67; Gaps 7;  
Matches 44; Conservative 18;  
QY 5 RSQRRRG-RRGEPGTALLVPLALGLGLALACLGLLAVVSLGSRASLSAQEPAQEELVAE 63  
DB 26 RSHRRQSCSVARVGLGLLL-LMGAGLAVQGFLLQLHWRLG-----EMV-- 69  
QY 64 EDQDPSLNQTEESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGDGAQ 123  
DB 70 -----TRLPDGPAGSWEQLIQERRS-----HEVNPAAHLTGAN 102  
QY 124 AGVDGTVSGWEERINSSPLRYNRQI-----GEFIVTRAGLYLYCOV 167  
DB 103 SSLTG-----SGPFLWETQLGLAFRLGLSYHDGALVVTKAGYIIYSKV 147

Search completed: April 12, 2003, 08:47:28  
Job time : 18 secs

QY 165 -----COMPHDEKAVYKLDLLVDGVLALRCLLEFSATASSLGQPLRLCOVYS-- 213  
 DB 167 DWQPEDRPMFAHFGQLRLHL-----PSATGEQTHLSLVAPG 204  
 QY 214 -----GLLALRGSSLRIT 228  
 DB 205 PGRPRDPLWQALITALSGGSASRLFT 232

RESULT 4  
 Q93JDI PRELIMINARY; PRT; 937 AA.  
 ID Q93JDI  
 AC Q93JDI  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Putative membrane protein.  
 GN STBAC16H6.31 OR SC05996 OR SCBAC16H6.31.  
 Streptomyces coelicolor.  
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 NCBI\_TaxID=1902;  
 [1] SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Collins M.R., Harris D.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."  
 RL Mol. Microbiol. 21:77-96(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 coelicolor A3(2)."  
 RL Nature 417:141-147(2002).  
 CC -!- SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).  
 DR EMBL; AL596162; CAC44610.1;  
 DR InterPro; IPR000408; Reg\_chromatins.  
 DR InterPro; IPR001680; WD40.  
 DR Pfam; PF00400; WD40.13.  
 DR PROSITE; PS00626; RCC1.2; UNKNOWN 1.  
 DR PROSITE; PS00678; WD REPEATS 1; UNKNOWN 5.  
 DR PROSITE; PS00082; WD REPEATS 2; 9.  
 DR PROSITE; PS00294; WD REPEATS\_REGION; 1.  
 KW Repeat; WD repeat.  
 SQ SEQUENCE 937 AA; 98790 MW; F14E4478A6B6B2F5 CRC64;

## Query Match

Best Local Similarity 7.4%; Score 94; DB 16; Length 937;  
 Matches 46; Conservative 19; Mismatches 64; Indels 52; Gaps 6;

QY 5 RSORRRGRGEPOTALLVPLALGLALALCLGLLAWLSGSRASLSAQEP-----A 56  
 DB 213 RSEGLDRTRNLRTARIVATLGCGLLVAS---TLSVAVLSRAEATRQDAVVOOLIT 269  
 QY 57 QEELVAEEDDPSELNPQTEESODPAP-----FLNRLVPRRS-----APKG 98  
 DB 270 QSSLLAERDPFAARLKALAARIDPSPETRFVLDAAVNPASGVLSHVPVDSVAFSPDG 329  
 QY 99 R-----KTRARRAIAAHE-----VHPRQDGAQAGVDCGTGSGWEE 135  
 DB 330 RTVASGSDGVVRWMTGTQRTAGRPLIGHHQITSIAFAPDGTILASSGFGDTGLWDL 389  
 QY 136 A 136  
 DB 390 A 390  
 RESULT 5  
 Q9RJ01 PRELIMINARY; PRT; 776 AA.  
 ID Q9RJ01  
 AC Q9RJ01  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Putative cation-transporting ATPase.  
 GN SCO0164 OR SCU1.13.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Seeger K.J., Harris D.;  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RX MEDLINE=97000351; PubMed=8843436;  
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."  
 RL Mol. Microbiol. 21:77-96(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 coelicolor A3(2)."  
 RL Nature 417:141-147(2002).  
 DR EMBL; AL109962; CABS3131.1;  
 DR InterPro; IPR00106; AATRNA\_ligaseII.  
 DR InterPro; IPR001757; ATPase\_EI-E2.  
 DR Pfam; PF00122; EI-E2 ATPase; 1.  
 DR Pfam; PF00702; Hydrolase; 1.  
 DR PRINTS; PR00119; CATATPASE.  
 DR PROSITE; PS00339; AA TRNA\_LIGASE II 2; UNKNOWN 1.  
 DR PROSITE; PS00154; ATPASE\_EI\_E2; UNKNOWN 1.

SQ SEQUENCE 776 AA; 80626 MW; 3E2C4D66D24ECB7D CRC64;

Query Match 7.4%; Score 93.5; DB 16; Length 776;  
 Best Local Similarity 24.1%; Pred. No. 8.5; Indels 65; Gaps 11;  
 Matches 63; Conservative 30; Mismatches 103

QY 12 RRGCGTALLVPLALGLGLALA--CLGLLLA-VVSLGSRASLSAQEPAPQELVAEEDQDP 68  
 DB 73 RRGHGVDLTAVLALGGLTLAGVGLAGVLLALMLATGRTLEGGAQRASHDLHALLAHAP 132  
 QY 69 SELNPTQESQDPAPFLNRLVRRSPAPKGRKTRARRAIAAHYEVHVRPQDGAQAGVDG 128  
 DB 133 RSARRRTGDC-----VVR-----VPLSEITAGDALVVGPGVWP-----VDG 169  
 QY 129 TVSGWE---EARNSSSPRYNRQICE---FIVTRAGLYLYCQVHFDGKAVYLLKLDL 181  
 DB 170 RVSTEAVLDESVLVTGPELQVTRQGEARGAGVAGGAFDL-----RATAEQDS 220  
 QY 182 LVGVLARCLCEFSATAASSLGQPLRLCO-----VSGLLALRPGSSLR----- 225  
 DB 221 TYAGIVRL-----AQQGAESAPVRLADRYAAWFLPALATAALAWLVGSAVRVAV 274  
 QY 226 -ITRLPWAHLKAAPFLTYFGL 245  
 DB 275 LVVATPCPLLLAAPVAVVSGL 295

RESULT 6  
 Q9AAB9 ID Q9AAB9 PRELIMINARY; PRT; 378 AA.  
 AC Q9AAB9  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hlyd family secretion protein.  
 GN CC0683.  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;  
 OC Caulobacter.  
 OX NCBI\_TaxID=155892;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RX MEDLINE=21173698; PubMed=11259647;  
 RA Nierman W.C.; Feldblyum T.V.; Laub M.T.; Paulsen I.T.; Nelson K.E.,  
 RA Eisen J.; Heidelberg J.F.; Alley M.R.K.; Ohta N.; Maddock J.R.,  
 RA Potocka I.; Nelson W.C.; Newton A.; Stephens C.; Phadke N.D.; Ely B.,  
 RA DeBoy R.T.; Dodson R.J.; Durkin A.S.; Gwinn M.L.; Haft D.H.,  
 RA Kolonay J.F.; Smit J.; Craven M.B.; Khouri H.; Shetty J.; Berry K.,  
 RA Uterback T.; Tran K.; Wolf A.; Vamathevan J.; Ermolaeva M.; White O.,  
 RA Salzberg S.L.; Venter J.C.; Shapiro L.; Fraser C.M.;  
 RT "Complete genome sequence of Caulobacter crescentus."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 DR EMBL; AE005743; AAK22668.1; -.  
 DR TIGR; CC0683; -.  
 DR InterPro; IPR003997; RtxD.  
 DR PRINTS; PR01490; RYTOXIND.  
 KW Complete proteome.  
 SQ SEQUENCE 378 AA; 39659 MW; 8B8818C437C15CBC CRC64;

Query Match 7.3%; Score 93; DB 16; Length 378;  
 Best Local Similarity 25.6%; Pred. No. 3.8;  
 Matches 68; Conservative 28; Mismatches 98; Indels 72; Gaps 12;

QY 9 RRGRR---GEPGTALLVPLALGLGLALACIGLLLVVSLGSRASLSAQEPAPQELVAE 63  
 DB 50 REGDRVVGQPIATLTLSALEGSDSFVLSR-----SLGAQSSAAGSRAAATQAALAE 104  
 QY 64 EQQDSELNPTQESQDPAPFLNRLVRRSPAPKGRKTRAR-----RAIAAHYEVHVP 115  
 DB 105 SRQ-----LITORAALNRELAERKSLALQTERLTLARAEEVARAETIAAQGLFSP 154  
 QY 116 RPOQDQAQAGVDGTGSGWEARINSSSPRYNRQICEFIVTRAGLYLYCQVHFDGKAV 175

DB 155 RE---LQARRSAELAVQOEASTLSSQALSVERQIGEV-----DARLA 193  
 QY 176 YKLKLDL---LVGVLARCLCEFSATAASSLGQPLRLCOVSGLLA----- 217  
 DB 194 APLDLQARAEAASTAGLEQ-QATQVEAQGRYVVVATVAGRVAALPVEAGQTVGVGAA 252  
 QY 218 ---LRPGSSLRIRTLFWAHLKAAPFL 240  
 DB 253 VAVLTPGDSALVAEL-YAPSRAGFV 277

RESULT 7  
 Q925J8 ID Q925J8 PRELIMINARY; PRT; 707 AA.  
 AC Q925J8  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Protein kinase mitogen-activated 8 interacting protein.  
 GN MAPK8IP OR PRKX8IP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ILS;  
 RA Ehringer M.A.; Thompson J.; Conroy O.; Xu Y.; Yang F.; Canniff J.,  
 RA Beeson M.; Gordon L.; Bennett B.; Johnson T.E.; Sikela J.M.;  
 RA "High-Throughput Sequence Identification of Gene Coding Variants  
 RT within Alcohol-Related QTLs";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF320076; AAK56104.1; -.  
 DR MGD; MGI:1309464; Mapk8ip.  
 DR InterPro; IPR000050; PID domain.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00640; PID; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR PROSITE; PS01179; PID; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Kinase.  
 SQ SEQUENCE 707 AA; 77381 MW; FDA53D891B6F5AA6 CRC64;

Query Match 7.3%; Score 92.5; DB 11; Length 707;  
 Best Local Similarity 23.3%; Pred. No. 9.3;  
 Matches 48; Conservative 19; Mismatches 76; Indels 63; Gaps 7;

QY 1 MAARRSRRRRGRCGPGTALLVPLALG-----LGLALA 33  
 DB 1 MAERESGLGRGAASPPAASPFLGLHIASPNFRLTHDISLEEFEDLSITDECGISLQ 60  
 QY 34 C---LGL-----LLAVVSLGSRASLSAQEPAPQELV-----AEEDQD----- 67  
 DB 61 CKDTLSLRPPRAGLLSAGSSGASRLQAELQWLMDLDAAGDTFCAEDDEEDELAAQ 120  
 QY 68 -PSELNPTQESQDPAPFLNRLVRRSPAP---KGRKTRARRAIAAHYEVHVRPQDGAQ 123  
 DB 121 RRGVGPAPKAESNQDPAP-----RSQGGPGTSGDTPYRKRPTLLNLFPOVPRSQDTLN 174  
 QY 124 AGVDGTGSGWEARINSSSPRYNRQ 149  
 DB 175 NNSLGLKXSHWODRVSRSSSPUKTGEQ 200

RESULT 8  
 Q8TET1 ID Q8TET1 PRELIMINARY; PRT; 977 AA.  
 AC Q8TET1  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE FLJ00093 protein (Fragment).

```

RA Parkhill J.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RP STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.F., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayar L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Uutterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
EMBL; Z93777; CAB07841.1; -.
DR EMBL; AE007002; AAK45514.1; -.
DR TIGR; MT1257; -.
DR TubercuList; Rv1219c; -.
DR InterPro; IPR001647; HTH_Tetr.
DR Pfam; PF00440; tetr; 1.
KW DNA-binding; Hypothetical protein; Transcription regulation;
KW Complete proteome.
SQ SEQUENCE 212 AA; 23181 MW; 8FBC03B909EA88C0 CRC64;

Query Match 7.2%; Score 91.5; DB 16; Length 212;
Best Local Similarity 24.5%; Pred. No. 2.5;
Matches 53; Conservative 26; Mismatches 78; Indels 59; Gaps

QY 11 GRGEGCTALLVPLALGLGL-----ALACLGLLAVVSLGSRASLSAQBPQAQELVAEE-- 64
DB 21 GRHG-----FGVGLRAIAEAGVSAALVIHHFGSKEGL---RKACDFFVAEEIR 66
QY 65 -----DQDPSLNPQTEESQDPAPFLNLRVRRRSGAPKGRKTRARRAIAAHYEVHPR 116
DB 67 SSKAAALKNSDPTTWLAQWAEIESVAPLMAYLVRSWGGELAKMLQWQMI----- 117
QY 117 PGDGAQAGVDGTGSGWEFARINSSPLRYNQIGEFI-VTRAGLYIYVCQVHFD----- 170
DB 118 -----DNAEEYLD-----EGVRAGTVKPSRDPRARARFLAITGGGFLLYLQWHNPDTLR 168
QY 171 -----EGKAVYVKDLLVDGVLAIRCL-EEFSATA 199
DB 169 AALRDYAHDMWLPSUEVYTEGLLADRAMYEAFLAEA 204

RESULT 10
Q937L3 PRELIMINARY; PRT; 1100 AA.
AC Q937L3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE SMC protein.
GN SMC.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RA Cobbe N., Heck M.M.S.;
RT "Phylogenetic analysis of SMC proteins.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ417688; CAD10418.1; -.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR003405; SMC_C.
DR InterPro; IPR003395; SMC_N.
DR Pfam; PF02463; SMC_C; 1.
DR Pfam; PF02463; SMC_N; 1.
SQ SEQUENCE 1100 AA; 118812 MW; 9800A265FB71BC2F CRC64;

Query Match 7.1%; Score 90.5; DB 2; Length 1100;

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Best Local Similarity 26.7%; Pred. No. 24;
Matches 55; Conservative 23; Mismatches 73; Indels 55; Gaps 8;

Qy 50 LSAQPA---QEELVAREDDQPSSELPQTESQDPAPFLNLRVPRSPAKGR----- 99
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 698 LSAQTRSLRSHRDETARLDAARLPVPTEDATPAELESALWQARQQAETGRAAREA 757
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 100 -----KT-RARRAIAAHYEVHPRPGDGA---QAGVD-----G 128
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 758 LEALALARELDTAWKTYRAAEARAALRERLRVNDASAAQGGDLDAAAAEVARREAAIG 817
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 129 TVSGHEEARINS---SSPLRYNRQIGEFIVTRAGLYLYLCVHFDEGKAVYKLDLLVDG 185
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 818 TLDEQEFPRAEAREAAALAYANLGEQNKVGRLLDLRLVLIARREGSA-----EPIDG 872
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 186 VLALRCLEFSATAASS-----LGP 205
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 873 CSPPGTKPKEWTAELARARAEIDLGP 898
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

:RESULT 11
:FTN7
ID Q9FTN7 PRELIMINARY; PRT; 522 AA.
AC Q9FTN7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE Putative Rer1a protein (ATRERIA).
OS P0005A05.12.
GN Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone:P0005A05."
RL EMBL; AP002863; BAB16908.1; -.
DR InterPro; IPR004932; Rer1.
DR Pfam; PF03248; Rer1; 1.
SQ SEQUENCE 522 AA; 58171 MW; AE43E294DFE88E7F CRC64;

Query Match 7.0%; Score 89; DB 10; Length 522;
Best Local Similarity 26.5%; Pred. No. 13;
Matches 78; Conservative 32; Mismatches 74; Indels 110; Gaps 21;

Yy 47 RASLSAQ---EPAQBELV--AEEDQPSSELPQTES-QDPAP-----FLN--- 86
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 93 RVSVNAQRKKERKHEIIVTSAEKDRGGTVRKXKESKEDPSGPIQHQIFQSIYFNIIHA 152
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 87 -----RLVRPR-----SAPKGRKTRAR 105
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 153 SGKKKVTVHACTVLSKDTSSRRRLEREGRHPASHLIGIGIVLVLGISSSKREGCFAR 212
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 106 AIAAHYEVHP---RPG--QNGA---QAGVDGTVSGWE-----EARINSSSPLRYNRQ 149
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 EVA-----SPSGFRPGFSGMDGADSGTAGAAAAAKWRTDASAFQYLDRTPTATGW 268
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 150 IGEFIVTRAGLYLYCQVHFDE-----GKAVYKLDLLVDGVIALRCLEFSATAASS 202
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 269 ICTLAV--AAIALV--RVYLQGVFIVTVYGLGIL-LNELLI-GFLSPMDPEARA-AASS 321
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 203 LCPQLRLCQVSGLLALRPGSSIRITLP-----WAHLKA---APFLTYEGLFQV 248
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 DGPAL---PTRGSDEFKP-----FIRRLPEKFWYATTKAFLIAFVMTFFSVFDV 368
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
Q9HYT9
```

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ID Q9HYT9 PRELIMINARY; PRT; 664 AA.
AC Q9HYT9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE Hypothetical protein PA3305.
GN PA3305.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Raizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
EMBL; AE004753; AAC06693.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 664 AA; 73136 MW; 19EBEF3098D1F4E CRC64;

Query Match 7.0%; Score 89; DB 16; Length 664;
Best Local Similarity 26.0%; Pred. No. 18;
Matches 70; Conservative 26; Mismatches 109; Indels 64; Gaps 10;

Qy 10 RGRGEGPTALLVPLALGLALCLGLLLAVLSGRSLASQEPQEE-----LVAE 63
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 224 RGRRRAGALLSRDLLSL-----LRTARGVARQARLSEEEERRVERWLAAASAL 275
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 64 EDQPSSELPQTESQDPAPFLNLRVPRSPAKGRKTRARRAJAAHYEVHPRPGDGAQ 123
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 276 EGTDPASMQALREELAQA-----VEPQWSNDQ-RYLLTRCSVLLKAVN-----AE 321
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 124 AGVDGTVSGMEEARINSSSPLRYNR--QIGEFIVTRAGL-----YLYL----- 164
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 KGMRAVASGEVEGRVGSAGTSLSWHRDLQMALFYCTRSALALLGLSVYIYTAWPAASGAM 381
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 165 -----QVHDEGKAVYKLDLLVDGVIALRCLEFSATAASSLGPQLRLCQVSG--LL 216
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 382 LLAAVWCSLFANRDNAVAIGLSFLRGIVYAI-----PAAMLVSQWLLPQWNGPPLL 432
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 217 ALRPGSSIRITLPWAHLKAAPFLTYEGL 245
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 433 *CLAMGVPLFFATLGMVAVPTAGTATSAI 461
||| : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
Q9F2P0 PRELIMINARY; PRT; 854 AA.
ID Q9F2P0;
AC Q9F2P0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Putative ABC transport system integral membrane protein.
GN SC03110 OR SCE41.19C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D.C., Harris D.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
```





CC activators or agonists, are used to treat a deficit of TREPA, e.g. to  
CC promote wound healing or tissue grafting, by promoting vascularisation,  
CC also to induce apoptosis for treating cancer and eliminating autoreactive  
CC T cells, as an adjunct to cancer chemotherapy or antiviral treatment.  
CC TREPA peptides can also be used to target cytotoxic agents or for  
CC affinity isolation of the corresponding receptor, the nucleic acid for  
CC which can be used to transform tumour cells to render them more  
CC responsive to TREPA and to screen for TREPA mimics.  
CC Ribozymes, antisense RNA, antibodies or peptides, are used to treat  
CC TREPA-associated diseases, e.g. tumours and metastases (by inhibiting  
CC vascularisation), inflammation or a wide range of autoimmune conditions,  
CC conditions involving abnormal stimulation of epithelial cells (e.g.  
CC atherosclerosis), for birth control (inhibiting ovulation and placental  
CC formation) or other angiogenic conditions (e.g. ulcers).  
XX  
XX  
SQ Sequence 189 AA;

Query Match 62.5%; Score 792; DB 19; Length 189;  
Best Local Similarity 99.3%; Pred. No. 1.1e-71;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 97 KGRKTRARRAIAAHYEVHPRPGDGAQAGVDGTVSGWEARINSSPLRYNRQIGEIFVT 156  
DB 37 KGRKTRARRGIAAHYEVHPRPGDGAQAGVDGTVSGWEARINSSPLRYNRQIGEIFVT 96  
QY 157 RAGLYLYLCQVHFDEGKAVYKLDLLVDGVLALRCLEFSAATAASSLGPQLRLCQVSGLL 216  
DB 97 RAGLYLYLCQVHFDEGKAVYKLDLLVDGVLALRCLEFSAATAASSLGPQLRLCQVSGLL 156  
QY 217 ALRPGSSLRIRTLPAWHLKAAPFLTYFGLFQVH 249  
DB 157 ALRPGSSLRIRTLPAWHLKAAPFLTYFGLFQVH 189

RESULT 14  
AAE00892  
ID AAE00892 standard; Protein; 189 AA.  
XX  
AC AAE00892;  
XX  
XX  
DT 04-JUL-2001 (first entry)  
XX  
DE Human UL4flag TREPA soluble construct.  
XX  
KW Human; tumour necrosis factor; TNF; angiogenesis; wound healing; tumour;  
TREPA; TNF related endothelium proliferative agent; metastasis; grafting;  
vulnerable; HUVEC; human umbilical vein endothelial cell; UL4flag.

Homo sapiens.  
AA  
PN US6207642-B1.  
XX  
XX  
PD 27-MAR-2001.  
XX  
XX 26-JUN-1998; 98US-0105343.  
XX  
XX 12-FEB-1997; 97US-0798692.  
PR 10-FEB-1998; 98US-0021706.  
XX  
XX (ABBO ) ABBOTT LAB.  
PA  
XX  
XX  
PI Wiley SR;  
XX  
DR WPI; 2001-280760/29.

XX Inducing angiogenesis in mammal at desired sites for promoting wound  
XX healing, by administering soluble fragment of extracellular domain of  
PT tumor necrosis factor related endothelium proliferative agent protein  
PT -  
XX  
XX Example 2; Column 75-78; 53pp; English.  
PS  
XX The present invention relates to extracellular signal molecules,

CC particularly members of tumour necrosis factor (TNF) family molecules  
CC designated as TREPA (TNF related endothelium proliferative agent).  
CC Soluble biologically active TREPA are used to treat TREPA-associated  
CC diseases, tumours or metastases. TREPA is used for inducing angiogenesis  
CC in human for promoting wound healing and for vascularising grafted  
CC tissue for successful grafting and to promote tissue grafts. The present  
CC amino acid sequence is human UL4flag TREPA soluble construct. This  
CC sequence which is a biologically active molecule is capable of inducing  
CC proliferation in HUVEC (human umbilical vein endothelial cells).  
XX  
XX  
SQ Sequence 189 AA;

Query Match 62.5%; Score 792; DB 22; Length 189;  
Best Local Similarity 99.3%; Pred. No. 1.1e-71;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 97 KGRKTRARRAIAAHYEVHPRPGDGAQAGVDGTVSGWEARINSSPLRYNRQIGEIFVT 156  
DB 37 KGRKTRARRGIAAHYEVHPRPGDGAQAGVDGTVSGWEARINSSPLRYNRQIGEIFVT 96  
QY 157 RAGLYLYLCQVHFDEGKAVYKLDLLVDGVLALRCLEFSAATAASSLGPQLRLCQVSGLL 216  
DB 97 RAGLYLYLCQVHFDEGKAVYKLDLLVDGVLALRCLEFSAATAASSLGPQLRLCQVSGLL 156  
QY 217 ALRPGSSLRIRTLPAWHLKAAPFLTYFGLFQVH 249  
DB 157 ALRPGSSLRIRTLPAWHLKAAPFLTYFGLFQVH 189

RESULT 15  
AAE00895  
ID AAE00895 standard; Protein; 146 AA.  
XX  
AC AAE00895;  
XX  
XX  
DT 04-JUL-2001 (first entry)  
XX  
DE Human TREPA (TNF related endothelium proliferative agent) fragment.  
XX  
KW Human; tumour necrosis factor; TNF; angiogenesis; wound healing;  
TREPA; TNF related endothelium proliferative agent; tumour; metastasis;  
grafting; vulnerary.

Homo sapiens.  
OS  
PN US6207642-B1.  
XX  
XX 27-MAR-2001.  
PD  
XX 26-JUN-1998; 98US-0105343.  
XX  
XX 12-FEB-1997; 97US-0798692.  
PR 10-FEB-1998; 98US-0021706.  
XX  
XX (ABBO ) ABBOTT LAB.  
PA  
XX  
XX  
PI Wiley SR;  
XX  
XX WPI; 2001-280760/29.

XX Inducing angiogenesis in mammal at desired sites for promoting wound  
XX healing, by administering soluble fragment of extracellular domain of  
PT tumor necrosis factor related endothelium proliferative agent protein  
PT -  
XX  
XX Example 14; Fig 1; 53pp; English.  
PS  
XX The present invention relates to extracellular signal molecules,  
CC particularly members of tumour necrosis factor (TNF) family molecules  
CC designated as TREPA (TNF related endothelium proliferative agent).  
CC Soluble biologically active TREPA are used to treat TREPA-associated  
CC diseases, tumours or metastases. TREPA is used for inducing angiogenesis  
CC in human for promoting wound healing and for vascularising grafted

CC tissue for successful grafting and to promote tissue grafts.  
CC The present amino acid sequence is human TREPA fragment.

XX  
SQ Sequence 146 AA;  
Query Match 60.0%; Score 761; DB 22; Length 146;  
Best Local Similarity 100.0%; Pred. No. 1e-68;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 104 RRATAAHVEVHPRPGDGAQAGVDGTVSGWEARINSSPLRYNRQICEFIVTRAGLYYL 163  
Db 1 RRATAAHVEVHPRPGDGAQAGVDGTVSGWEARINSSPLRYNRQICEFIVTRAGLYYL 60  
Qy 164 YCOVHFDEGKAVYLKLDLLVDGVLAALRCLEEFSAATAASSLGPQLRLCOVSGLLALRPSS 223  
Db 61 YCOVHFDEGKAVYLKLDLLVDGVLAALRCLEEFSAATAASSLGPQLRLCOVSGLLALRPSS 120  
Qy 224 LRIRLTPWAHLKAAPFLTYFGLFQVH 249  
nb 121 LRIRLTPWAHLKAAPFLTYFGLFQVH 146

Search completed: April 12, 2003, 08:39:00  
Job time : 38 secs

```

RT sporulation genes."
RL Microbiology 142:3103-3111(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borrias R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Goleightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Kluerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue J.C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Pressecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -----
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CC -----
CC EMBL; D84432; BA012474.1; --
CC EMBL; Z99117; CAB14479.1; --
CC Subtilist; BGI1652; YqfB.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 3 23 POTENTIAL.
SQ SEQUENCE 139 AA; 15740 MW; 60C7F38CDB1F4CB7 CRC64;
Query Match 6.8%; Score 86; DB 1; Length 139;
Best Local Similarity 27.8%; Pred. No. 1.6;
Matches 30; Conservative 18; Mismatches 46; Indels 14; Gaps 3;
QY 33 ACGLGLLAVSLGSRSLAQEPAEELVAEEDDPSELNPQTEESQD--PAPELNLVR 90
DB 13 AIIIGTSAIFGKSK-----EKQNSQKRRKPOHVOSAPQKQSKEDAPAPIENRMVQ 66
QY 91 PRSAPKGRKTRAR-----RAIAAHYEHVPRPGDGAQAGVDGTGSG 132
DB 67 ARREAERRETARNLKGLELDLAAAKQKTVYTKQKMLQYNKDTVVQS 114

```

Search completed: April 12, 2003, 08:39:19  
Job time : 15 secs

15-JUN-2002 (Rel. 41, Last annotation update)  
 Lymphotoxin-alpha precursor (LTA-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1).  
 LTA OR TNFSF1 OR TNFB.  
 GN Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 NCBI\_TaxID=9986;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=91065534; PubMed=2249779;  
 RA Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V., Andreyeva A.V., Nedospasov S.A.;  
 "Cloning and structural analysis of genes coding for tumor necrosis factor and lymphotoxin in rabbits.";  
 Mol. Biol. (Mosk) 23:1743-1750(1989).  
 CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to TNFSF1A/TNFR1, TNFRSF1B/TNFR and TNFSF14/HVEM. In its heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is produced by lymphocytes and cytotoxic for a wide range of tumor cells in vitro and in vivo.  
 CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one LTA subunits or (less prevalent) two LTA and one LTB subunits (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane protein (heterotrimers) (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC  
 EMBL; X55745; CAA39275.1; ALT\_SEQ.  
 EMBL; M60340; AAA31483.1; -.  
 EMBL; M60341; AAA31485.1; -.  
 PIR; JH0309; JH0309.  
 PIR; P00998; P00998.  
 DR HSSP; P01374; 1TNR.  
 DR InterPro; IPR003636; TNF\_abc.  
 DR InterPro; IPR000478; TNF\_family.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISCT.  
 DR ProDom; PD002012; TNF\_abc; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF; 1; 1.  
 DR PROSITE; PS0049; TNF; 2; 1.  
 KW Cytokine; Glycoprotein; Cytotoxin; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 197 LYPHOTOXIN-ALPHA.  
 FT CARBOHYD 88 N-LINKED (GLCNAC...), (POTENTIAL).  
 SQ SEQUENCE 197 AA; 21126 MW; 0CF18CC9B5E2345 CRC64;  
 Query Match 6.9%; Score 87; DB 1; Length 197;  
 Best Local Similarity 23.7%; Pred.No. 1.9;  
 Matches 61; Conservative 24; Mismatches 82; Indels 90; Gaps 11;  
 QY 16 PGTALLVPLALGLALACGLGLLAVVSLGSLASLSAQEP-----AQBELVAEEDQDPS 69  
 DB 3 PGRRLVPL-----LLGLLLAPPPGACGLPGAEFPSPSARNAQRL--QKHFGHS 51

QY 70 ELNPQTEESQDPAPFLNRLVRRRSAPKGRKTRAR--RAIAAHYEVHPRPGQGAQGVND 127  
 DE factor ligand superfamily member 1).  
 DB 52 TLKPAALVGD-----SAQDSLWRANTDRAFLRH----- 82  
 QY 128 GTVSGWEARINSSSPURYNRQIGEFIVTAGLYLYCYQVHFD-EG---KAVYVKLDLLV 183  
 DE Lymphotoxin-alpha precursor (LTA-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1).  
 DB 83 -----GFSLSNNSLLVPSGLYFVYSQVVFSGEGSPKAVPTPLYLAAH 125  
 QY 184 DGVLAALRCLEEFSA-----TAASSL-----GPOLRLCQVSGLLALRPGSSLRITL 229  
 DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=94083525; PubMed=8260599;  
 RX Cludts I., Cleuter Y., Kettmann R., Burny A., Droogmans L.;  
 "Cloning and characterization of the tandemly arranged bovine lymphotoxin and tumour necrosis factor-alpha genes.";  
 RT Cytokine 5:336-341(1993).  
 CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to TNFSF1A/TNFR1, TNFRSF1B/TNFR and TNFSF14/HVEM. In its heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is produced by lymphocytes and cytotoxic for a wide range of tumor cells in vitro and in vivo.  
 CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one LTA subunits or (less prevalent) two LTA and one LTB subunits (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane protein (heterotrimers) (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC  
 EMBL; Z14137; CAA78510.1; -.  
 PIR; S24641; S24641.  
 DR HSSP; P01374; 1TNR.  
 DR InterPro; IPR003636; TNF\_abc.  
 DR InterPro; IPR000478; TNF\_family.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISCT.  
 DR ProDom; PD002012; TNF\_abc; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF; 1; 1.  
 DR PROSITE; PS0049; TNF; 2; 1.  
 KW Cytokine; Glycoprotein; Cytotoxin; Signal.  
 FT SIGNAL 1 33  
 FT CHAIN 34 204 LYPHOTOXIN-ALPHA.

```
CC -1- DEVELOPMENTAL STAGE: Low levels at prenatal stage E15, increased  
CC levels during the first postnatal days, with a plateau at  
CC postnatal day 15.  
CC -1- INDUCTION: Upon neuron differentiation.  
CC -1- PTM: Phosphorylated by JNK in differentiated cells.  
CC -1- SIMILARITY: BELONGS TO THE JIP SCAFFOLD PROTEINS FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 PID DOMAIN.  
CC -----  
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CC or send an email to license@sib-sib.ch).  
CC -----  
DR ENBL; AF003115; AAB66317.1; -;  
DR ENBL; AF109768; AAD38346.1; -;  
DR ENBL; AF109769; AAD38347.1; -;  
DR ENBL; AF109770; AAD38348.1; -;  
DR ENBL; AF109771; AAD38349.1; -;  
DR ENBL; AF054611; AAD22580.1; -;  
DR TRANSFAC; T04458; -;  
DR MGD; MGI:l309454; Prkm8ip.  
DR InterPro; IPR000050; PID_domain.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00018; SH3; 5.  
DR Pfam; PF00640; PID; 5.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS01179; PID; 1.  
DR PROSITE; PS50002; SH3; 1.  
DR SH3 domain; Alternative splicing; Phosphorylation.  
KW SH3 domain; ASP/GLU-RICH (ACIDIC).  
FT FT DOMAIN 41 47 ASP/GLU-RICH (ACIDIC).  
FT FT DOMAIN 107 116 ASP/GLU-RICH (ACIDIC).  
FT FT DOMAIN 127 281 JNK-BINDING DOMAIN (JBD).  
FT FT DOMAIN 355 359 POLY-PRO.  
FT FT DOMAIN 484 545 SH3.  
FT FT DOMAIN 557 696 PID.  
FT FT VARSPLIC 1 33 MAERESGLGGAASPPAASPFLGHITASPNER -> MOLV  
FT FT LKWDSPDNDSDWLEDQWEHW (IN ISOFORM JIP-1C  
FT FT AND ISOFORM JIP-1D).  
FT FT MISSING (IN ISOFORM JIP-1E).  
FT FT MISSING (IN ISOFORM JIP-1D).  
FT FT MISSING (IN ISOFORM JIP-1A).  
FT FT PG-> A (IN REF. 2).  
FT FT R -> RP (IN REF. 2).  
SQ SEQUENCE 707 AA; 77281 MW; 274013B12D91049D CRC64;  
  
Query Match 7.1%; Score 90; DB 1; Length 707;  
Best Local Similarity 26.5%; Pred. No. 4-9;  
Matches 40; Conservative 16; Mismatches 59; Indels 36; Gaps 6;  
  
QY 29 GLALAC---LGL-----LLAVVSLGRASLSAQEAQLV-----AEEDQD---- 67  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
DB 56 GISLOCKDTLSLRPPRAGLLSAGSSGSAGSRLOAEMQLMDLDAAGDTPGAEDDEEEEDD 115  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
QY 68 -----PSELNPOTESQDPAPFNLRVPRRSAP----KGKTFARRAIAAHVEVHPRG 118  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
DB 116 ELAAQRFGVGVPKAENQDPAP-----RSQGQPGTGSGDTVRPKPTTLNLPFQVPRS 169  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
QY 119 QDGAQAGVDGTGVSGWEARINSSSPLRYNRQ 149  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
DB 170 QDTLNNSLGKKHSWQDRVSRSSSPLKTGEQ 200  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
  
RESULT 10  
TNFB_RABIT STANDARD; PRT; 197 AA.  
ID TNFB_RABIT  
AC F10154;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)
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